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Pred. No. is the number of results predicted by chance to have a

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REFERENCE AUTHORS TITLE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	rocus	S82226	RESULT 1
1 (bases 1 to 585) **Cones:D::_Brunovskis;P::_Witter;R:_and_Kung;H:J: **Retroviral-insertional-activation-in-a-herpesvirus:-transcriptional	Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Marek's disease-like viruses.	Gallid herpesvirus 2	Gallid herpesvirus 2	•	S82226.1 GI:1839499	\$82226	Genomic DNA, 585 nt].	{RS region, intervening sequence} [Marek's disease virus MDV, RM1,	S82226 585 bp DNA linear VRL 12-FEB-1997		

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Reticuloendotheliosis virus 713 proviral clone RNA.

M2223 M1059 M1672

M2223.1 GI:209708

Ing terminal repeat (LTR).

Reticuloendotheliosis virus

Reticuloendotheliosis virus

Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.

1 (bases 99 to 195)

Ridgway,A.A., Swift,R.A., Kung,H.J. and Fujita,D.J.

In vitro transcription analysis of the viral promoter involved

C-myc activation in chicken B lymphomas: detection and mapping
                                                                                                                                                                                                                                                                                             361
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Authors indicate intervening sequence from nt 23 to nt 555 inclusive derived from co-infecting reticuloendotheliosis v
                                                                                                                                                                                          CCTACTGGGTGGGGTAGGGATCCGGACTGAATCCGTAGTATTTCGGTACAACA
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/mol_type="genomic DNA"
/db_xref="taxon:10390"
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B-lymphoma induction by reticuloendotheliosis virus: characterization of a mutated chicken syncytial viru involved in c-myc activation
J. Virol. 61 (7), 2084-2090 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Original source text: Reticuloendotheliosis virus
line 151-5 B lymphomas), cDNA to mRNA, clone 713.
Location/Qualifiers
                                                                                                                                  CGGACTGAATCCGTAGTATTTCGGTACAACA
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Swift,R.A., Boerkoel,C.,
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/mol type="genomic RNA"
/db xref="taxon:11636"
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Pred. No. 2.9e-145;
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Hertig, C.H., Coupar,
Direct Submission
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Hertig,C., Coupar,B.E., Gould,A.R. and Boyle,D.B.
Field and vaccine strains of fowlpox virus carry integrated
sequences from the avian retrovirus, reticuloendotheliosis virus
Virology 235 (2), 367-376 (1997)
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Location/Qualifiers
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Fowlpox virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="gag"
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PAIAEEGEEGQOPDSTVMASPPHTRSGLEFGAQGPSGMYPLRETGERDMGGRPMRTYV
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RTESRREVRNDGGVQVTDEREIEAQFPATREDWDPMTGRGNDNLERFXQTLLRGLRAA
ARKETNLSKLTEVRQCADESPFAYLERLYQAYRTWSPIDPRAPENQAAIVILAQESRAE
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ASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLL
PVRKSGTSEYRWQDLEBVNKRVETIHFTVPNPYTLLSLPPDRIWYSVLDLKDAFFC
PVRKSGTSEYRWQDLEBVNKRVETIHFTVPNPYTLLSLPPDRIWYSVLDLKDAFFC
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1812. .3
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FIEISKQRCFSIKVTDSTYLYIENRTMSYSISTSHDKNEPYEKGIIMMNIECYFVA
CLEGGGCTVNVHLGDROISDNISESGGFLMDVNTDHVIDTKYVGLFITKIKVDAHVGYG
QNVIMFPEKNLFSQTNGFNFILYDITVQDRNVLLLITSKYIYNLCDDKYYDIFELKYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="standard vaccine strain from Cyanamid-Webster Pty
Ltd, Castle Hill, New South Wales, Australia.
EcoRI/PstI 4.3kb fragment from the 9.8kb PstI genome
                                                                                                                                                                                                                                                                                                                                                       /gene="pro/pol"
<3312. .>4292
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                                                                                                                                                                                                                                                                                                                        gene="pro/pol"
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1812. .3311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
/protein_id="AAC58238.1"
/db_xref="GI:2393893"
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/mal_type="genomic DNA"
/strain="S (standard vaccine strain)"
/db_xref="taxon:10261"
                           !PLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKKSPTLFDEALNRDLQ!
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                                                                                                                                                     2 (bases 1 to 8221)
Singh,P., Schitzlein, W.M. and Tripathy,D.N.
Reticuloendotheliosis Virus Sequences Within the
Strains of Fowlpox Virus Display Variability
J. Virol. (2003) In press
                                                                                                                                                                                                                                                                                                                                                                                    b2Z1 bp DNA linear VRL 12-MAR. Fowlpox virus hypothetical protein gene, partial cds; integrate reticuloendotheliosis provirus, complete sequence; and protein kinase-like protein gene, partial cds.

AF246698
Direct Submission
Submitted (12-MAR-2003) University of Illinois at Urbana-Champaign,
2001 South Lincoln Avenue, Urbana, IL 61802, USA
                                                                                                                                                                                                                             (bases 1 to 8221)
Singh, P., Kim, T.-J. and Tripathy, D.
Re-emerging fowlpox: evaluation of
Avian Pathol. 29, 449-455 (2000)
                                                                                                                                                                                                                                                                                                  Fowlpox virus
Viruses; dsDNA viruses, no RNA stage; Poxviridae;
                                                             Submitted (16-MAR-2000) Veterinary Pathobiology, University Illinois, 2001 South Lincoln Avenue, Urbana, IL 61802, USA 4 (bases 1 to 8221)
                                               Schnitzlein, W.M., Singh, P.,
                                                                                                            Direct Submission
                                                                                                                       Schnitzlein, W.M., Srinivasan, V. and Tripathy, D.N.
                                                                                                                                                                                                                                                                                           Avipoxvirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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/product="gag_protein"
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/protein_id="AA062318.1"
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PAIAEBGEEGQOPDSTVMASPPHTRSGLEFGAQGPSGMYPLRETGERDMGGRPMRTYV
PFTTSDLYNMKNQNPSFSQAPDBVISLLESVFYTHOPFMDDCQOLLTLFTTERERRV
PRTSRREVRNDGVQVOTDEREIEAQFPSATTEDMDPMTGRGNDNLERYRQILLRGLRAA
ARKPINLSKITEVRQGADESPTAYLERLYQAYZTWSPIDPRAPENQAIVIQFVSQSA
PBIRKKIQKIDGFQGKSLSELVAIAQKVFDQREDPAKATHELTQKMAKVLLAQESRAE
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/protein_id="AAF81698.2"
/db_xref="GI:28927670"
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                                                                                                              codon_start=1
                                                                                                                                         note="env"
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/db_xref="GI:28927669"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
/product="hypochetical protein"
/protein id="AAA62317.1"
/db_xref="GI:28927671"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="NNDTSLPVAVKVIYGTVTI"
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/mol_type="genomic DNA"
/db_xref="taxon:10261"
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Location/Qualifiers
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ACRLTR2
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ACCESSION
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Best Local S
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ACRLTR2

Reticuloendotheliosis virus 71:
M22224 M10660 M16722

M22224.1 GI:209709

long terminal repeat (LTR).
Reticuloendotheliosis virus
Reticuloendotheliosis virus
Viruses; Retroid viruses; Retro
1 (bases 510 to 602)
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506;
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                                     TGAATCCGTAGTATTTCGGTACAACA 533
TGAATCCGTAGTATTTCGGTACAACA
                                                                                                                             CGTGCGGCCCAGATTCGAATCTGTAATAAAAGCTTTTTCTTCTATATCCTCAGATTGGCA
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                                                                                       CGTGCGGCCCAGATTCGAATCTGTAATAAAAGCTTTTTCTTCTATATATCCTCAGATTGGCA 447
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QDQIDSLAEVVLQNRRGLDLLTAEQGGICLALQBKCCFYANKSGIVRDKIRKLQBDLI
ARKRALYDNPLMNGLNGFLPYLLPLLGPLFGLILFLTLGPCIKTLTRIIHDKIQAVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="ORF 203"
/codon_start=1
/product="protein kinase-like protein"
/protein id="AAO62319.1"
/db_xref="GI:28927673"
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Retroviridae;

Gammaretrovirus

7 bp 713

ss-RNA line proviral clone

linear lone RNA.

VRL 27-APR-1993

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JOURNAL
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MEDLINE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B-lymphoma induction by reticuloendotheliosis virus: characterization of a mutated chicken syncytial virus involved in c-myc activation
J. Virol. 61 (7), 2084-2090 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ridgway, A.A., Swift, R.A., Kung, H.J. and Pujita, D.J.
In vitro transcription analysis of the viral promoter involved i c-myc activation in chicken B lymphomas: detection and mapping c two RNA initiation sites within the reticuloendotheliosis virus long terminal repeat
J. Virol. 54 (1), 161-170 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 About
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Original source text: Reticuloendotheliosis virus line 151-5 B lymphomas), cDNA to mRNA, clone 713.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 887)
Swift,R.A., Boerkoel,C., Ridgway,A., Fujita,D.J., Dodgson,J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kung, H.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                          TGTAAGCGGCTATATAAGCCAGGTGCATCTCTTGCTCGGGGTCGCCGTCCTACACATTGT
                                                                                                                                                                                                                                      TGTAAGCGGCTATATAAGCCAGGTGCATCTCTTGCTCGGGGGTCGCCGTCCTACACATTGT
                                                                                                                                                                                                                                                                             GCCAATGGTTGTAAAGGGCAGATGCTATCCTCCAATGAGGGAAAATGTCATGCAACATCC
                                                                                                                                                                                                                                                                                              GCCAATGGTTGTAAAGGGCAGATGCTATCCTCCAATGAGGGAAAATGTCATGCAACATCC
                                                                                                                                                                                                                                                                                                                                                 GCATCAGACCACTTGCACCATCCAATCACGAACAAACACGAGATCGAACTATCATACTGA
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                                                                                  CGGACTGAATCCGTAGTATTTCGGTACAACA 533
                                                                                                                                                                  TGTGACGTGCGGCCCCGATTCGAATCTGTAATAAAAGCTTTTTCTTCTATATCCTCAGAT
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/note="3' LTR"
805. .806
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|mol_type="genomic RNA"
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99.0%;
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Pred. No. 8.8e-144;
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                                                             188
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3 (bases 1 to 745)
Singh, P., Schnitzlein, W.M. and Tripathy, D.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 745)
Singh, P., Schnitzlein, W.M. and Tripathy, D.N.
Reticuloendotheliosis Virus Sequences Within
Strains of Fowlpox Virus Display Variability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 745)
Singh, P., Kim, T.-J. and Tripathy, D.N.
Re-emerging fowlpox: evaluation of isolates
Avian Pathol. 29, 449-455 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Powlpox virus TCP-Blen ORF201 gene, partial cds;
Reticuloendotheliosis virus remnant LTR, complete
protein kinase-like protein gene, partial cds.
AY255632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (13-MAR-2003) Veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Avipoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses, no RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fowlpox virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fowlpox virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           llinois at Urbana-Champaign,
                                                                                                                                            ATGCTTGCTTGCCTTAGCCGCCATTGTACTTGATATTTTCGCTGATATCATTTCTCGGA
                                                                                                                                                                                                           GGAGGGAGCTCCGGGGGGAATAGCGCTTGGCTAACTGCCATATTAGCTTCTGTAATC
AGACCACTTGCACCATCCAATCACGAACAAACACGAGATCGAACTATCATACTGAGCCAA
                    AGACCACTTGCACCCATCCAATCACGAACAAACACGAGATCGAACTATCATACTGAGCCAA
                                                             GGAGGGAGCTCCGGGGGAATAGCGCTGGCTGACTGCCATATTAGCTTCTGTAATC
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                                                                                                                                                                                                                                                                                                                                /note="ORF203; ORF2"
/codon_start=1
/product="protein kinase-like protein"
/protein_id="AAP21483.1"
/db_xref="G1:30267695"
/translation="MDIITNTTMFDIQFNDIPNIPYVDIEKPLLVYSC"
                                                                                                                                                                                                                                                                                                                                                                                                                                     643. .>745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/evidence=not_experimental
/product="ORF201"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 indentical to sequence in the vaccine strain Pox' (Vineland Laboratories, Vineland, NJ)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="vaccine strain TCP-Blen"
/db_xref="taxon:10261"
/note="from CEVA Laboratory, Overland Park,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Fowlpox virus"
mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="Reticuloendotheliosis virus proviral remnant LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="NNDTSLPVAVKVIYGTVTI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein_id="AAP21482.1"
db_xref="GI:30267694"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="hypothetical protein;
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99.4%;
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Pred. No. 5.1e-140;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                        DB 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.

1 (Dases 1 to 940)

Gabus-Darlix,C. and Darlix,J.

NOVEL INTERNAL RIBOSOME ENTRY SITE AND VECTOR CONTAINING
PATENT: WO 9849334-A 1 05-NOV-1998;

GABUS DARLIX CAROLINE (FR); INST NAT SANTE RECH MED (FR)

Location/Qualifiers
                             GAAAATGTCATGCAACA----TCCTGTAAGCGGCTATATAAGCCAGGTGCATCTCTTGC
                                                                                             AGATCGAACTATCATACTGAGCCAATGGTTGTAAAGGGCAGATGCTATCCTCCAATGAGG
                                                                                                                                                           ĠĀĀĀĀTGTĊĀTĠĊĀĀĆĀTCCTGTĊĊŦĠŦĀĀĠĊĠĠĊŦĀŦĀŦĀĀĠĊĊĀĠĠŦĠĊĀŤĊŦĊŦŦĠĊ
                                                                       AGAT CGAACTAT CATÁCTGAGC CAATGGTTGTAAAGGGCAGATGCTAT CCTCCAATGAGG
                                                                                                                                         GAAATGTTCGTTGGAGGCGAGCATCAGACCACTTGCGCCATCCAATCACGAGCAAACACG
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                                                                                                                                                                                                                                    -----ATCATTTCTCGGAATCGGCATCAGAGAGCAGGCTCATAAACCATAAAAG
                                                                                                                                                                                                                                                                            GTAATCATGCTTGCCTTAGCCGCCATTGTACTTGATATTTTCGCTGATATCATTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Reticuloendotheliosis virus"
/mol_type="unassigned DNA"
/strāin="TYPE A (REV-A)"
/isolate="LEADER 5' DE L'ARN GENOMIQUE :
/db_xref="taxon:11636"
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93.3%;
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Pred. No. 3.8e-124;
0; Mismatches 11;
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Best Local Sim
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INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE OS Reticuloendotheliosis virus
PN JP 2001500021-A/1
PD 09-JAN-2001
PP 20-ARR-1998 JP 199846672
PR 28-ARR-1997 FR 97/05203
PI MARCELO LOPEZ LASTRA, CAROLINE GABUS DARLIX, JEAN LUC DARL C12N15/86,C12N15/11/C12N15/67
CC Strandedness: Single;
CC Topology: Linear;
CC Topolog
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BD006232
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Viruses, Retroid viruses; Ret
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JP 2001500021-A/1.
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93.3%;
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Pred. No. 3.8e-124;
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Gammaretrovirus
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LUC DARLIX PC

/organism="Reticuloendotheliosis
/mol_type="genomic RNA"
/db_xref="taxon:11636" /organism='Reticuloendotheliosis virus'
Location/Qualifiers

Length 940;

GAAAATGTCATGCAACA----TCCTGTAAGCGGCTATATAAGCCAGGTGCATCTCTTGC AGATCGAACTATCATACTGAGCCAATGGTTGTAAAGGGCAGATGCTATCCTCCAATGAGG GAAATGTTTGTTGAAGGCAAGCATCAGACCACTTGCACCATCCAATCACGAACAACAACACG AGATCGAACTATCATACTGAGCCAATGGTTGTAAAGGGCAGATGCTATCCTCCAATGAGG GARATGTTCGTTGGAGGGAGCATCAGACCACTTGCGCCATCCAATCACGAGCAAACACG CTCGGAATCGGCÁTCÁTTTCTCGGAATCGGCATCÁAGAGCAGGCTCATAGACCATAAAAG GTAATCATGCTTGCCTTAGCCGCCATTGTACTTGATATATTTCGCTGATATCATTT 120 -----ATCATTTCTCGGAATCGGCATCAAGAGCAGGCTCATAAAACCATAAAAG GTAATCATGCTTGCCTTAGCCGCCATTGTACTTGATATATTTCGCTGAT-----AATGTGGGAĞĞAĞCTCCĞĞĞĞĞAĀTAĞCĞCTĞĞCTÇĞCTAACTĞCÇATATTAĞÇTTÇT AATGTGGGAGGGAGCTCCGGGGGGAATAGCGCTGGCTCGCTAACTGCCATATTAGCTTCT Indels 25; Gaps 300 302 240 242 180 182 134 60 81

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REFERENCE
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Location/Qualifiers
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Reticuloendotheliosis virus
Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
1 (bases 1 to 545)
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S70398
LTR, U3, R and U5 regions, long terminal repeats, provirus Reticuloendotheliosis virus A REV-A, A, Genomic RNA, 545 nt].
                                                                                                                                                                                                           GTAATCATGCTTGCCTTAGCCGTCATTGTACTTGATATTTTCGCTGATATCATTT
                                                                                                                                                                                                                             GTAATCATGCTTGCCTTAGCCGCCATTGTACTTGATATATTTCGCTGAT-----
TCGGGGTCGCCGTCCTACACATTGTTGTGACGTGCGGCCCAGATTCGAATCTGTAATAAA
                                     GAAAATGTCATGCAACA----TCCTGTAAGCGGCTATATAAGCCAGGTGCATCTCTTGC
                                                                                  AGATCGAACTATCATACTGAGCCAATGGTTGTAAAGGGCAGATGCTATCCTCCAATGAGG
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/mol_type="genomic RNA"
/db_xref="taxon:11636"
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93.1%;
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Pred. No. 7.6e-124;
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Query Match
Best Local Similarity
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Gallid herpesvirus 2
Viruses; dsDNA viruses,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Marek's disease-like viruses.
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TCGGGGTCGCCGTCCTACACATTGTTGTGACGTGCGGCCCAGATTCGAATTCTTAATAAA
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/mol_type="genomic DNA'
/db_xref="taxon:10390"
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. ORGANISM
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REXXX2
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Best Local 9
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                                                                                                                           341
                                                                                                                                                                                                                     415 CÁTGAÁCGGÁCÁCGAGÁTCGGÁCTATCATÁCTGGÁGCCÁATGGTTGTÁAÁAGGGCÁGÁTGC
                                                                                                                                                                                                     288
                                                                                                                                                                                                                                                                                                                                                        169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               424;
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1 (bases 1 to 859)
Shimotohno, K., Mizutani, S. and Temin, H.M.
Sequence of retrovirus provirus resembles that
transposable elements
transposable 5768), 550-554 (1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143
                            AGATTCGAATCTGTAATAAAAGCTTTTTCTTCTATATCCTCAGATTGGCAGTGAGAGGAG
                                                                                        CCAGGTGCATCTCTTGCTCGGGGTCGCCGTCCTACACA---TTGTTGTGACGTGCGGCCC
                                                                                                                                             TACTCTCCAATGAGGGAAAATGTCATGTAACACCCTGTAAGCTGTAAGCCGCTATATAAG
                                                                                                                                                                        TATCCTCCAATGAGGGAAAATGTCATGCAACATC-----CTGTAAGCGGCTATATAAG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Spleen necrosis virus
Viruses; Retroid viruses; Retroviridae; Mammalian
retroviruses; 1-Mammalian type C virus group.
1 (bases 1 to 859)
                                                                 cceseracarereriscrecises de la constant de la const
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Spleen
V01205
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                                                                                                                                                                                                                                              CACGAACAACACGAGATCGAACTATCATACT-GAGCCAATGGTTGTAAAGGGCAGATGC
                                                                                                                                                                                                                                                                                               ACAAACCACAAAAAGGAAACGCGCACCGAAGGCAAGCATCAGACCACTTGCGCCCATCCAAT 414
                                                                                                                                                                                                                                                                                                                          ATAAACCATAAAAGGAAATGTTTGTTGAAGGCAAGCATCAGACCACTTGCACCATCCAAT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spieen necrosis virus
V01205 J02389
V01205.1 GI:61794
                                                                                                                                                                                                                                                                                                                                                                           TGTACTTGĂTĂTGCCĂTTŤĊTĊGĠĀATCGGCATĆAAGTTTCGCTTCŤCGĀĠĀĠĊĀAĠĊĊĊ
                                                                                                                                                                                                                                                                                                                                                                                                              TGTACTTGATAT---ATTTCGCTGATATCATTTCTCGGAATCGGCATCAAGAGCAGCTC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GÉTGGÉCTACTGGGGGGGTAGGGATCCGGACTGAATCCGTAGTATTTCTGTACAACA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGGCCTACTGGGTGGGGTAGGGATCCGGACTGAATCCGTAGTATTTCGGTAGAACA 533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCTTTTT-CTTCTAFATCCTCAGAGTGAGTGAGAGGAGA-TTTTGTTCGTGGTGTTG 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Spleen necrosis
/mol_type="genomic DNA"
/db_xref="taxon:11836"
/note="cellular DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Spleen necrosis"
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|mol_type="genomic DNA"
|db_xref="taxon:11836"
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db_xref="taxon:11836"
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end) integrated in chicken cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               424;
                                                                                                                                                                                                                                                                                                                                                                   Spleen necrosis virus
Spleen necrosis virus
Viruses, Retroid viruses, R
retroviruses; 1-Mammalian t
1 (bases 1 to 891)
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Spleen necrosis virus (
V01204 J02388 M12296
V01204.1 GI:61793
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Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shimotohno, K., Mizutani, S. and Temin, H.M. Sequence of retrovirus provirus resembles that of transposable elements
                                                             TACT CTCA ATGAGGGAAAATGT CATGTAACAC CCTGTAAGCTGTAAGCGGCTATATAAG
                                                                                                                                                              CACGAACAACACGAGATCGAACTATCATACT-GAGCCAATGGTTGTAAAGGGCAGATGC
                                                                                          TATCCTCCAATGAGGGAAAATGTCAATGCAACATC-----CTGTAAGGGGCTATATAAG
                                                                                                                                       ACAAACCACAAAAGGAAACGCGCACCGAAGGCAAGCATCAGACCACTTGGGGCCATCCAAT
                                                                                                                                                                                                                                          ATAAACCATAAAAGGAAATGTTTGTTGAAGGCAAGCATCAGACCACTTGGACCATCCAAT
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                                                                                                                                                                                                                                                                                                                                TGTACTTGATAT---ATTTCGCTGATATCATTTCTCGGAATCGGCATCAAGAGCAGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 285 (5766), 550-554 (1980)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Gallus sp."
/mol_type="genomic DNA"
/db_xref="taxon:9036"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Gallus sp."
/mol_type="genomic DNA"
/db_xref="taxon:9036"
26...>891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/db_xref="taxon:11836"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Spleen necrosis virus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 313.8; DB 14;
Pred. No. 2.3e-85;
0; Mismatches 57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 16;
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287

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VERSION
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AF006066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 1022)
Hertig,C., Coupar,B.E., Gould,A.R. and Boyle,D.B.
Field and vaccine strains of fowlpox virus carry integrated sequences from the avian retrovirus, reticuloendotheliosis virus virology 235 (2), 367-376 (1997)
97428585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (30-MAY-1997) Division of Animal Health, Portarlington Road, Geelong, Victoria 3213, Austra-
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 1022)
Hertig, C.H., Coupar,
Direct Submission
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Fowlpox virus S envelope glycoprotein (env)
3, long terminal repeat, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fowlpox virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Avipoxvirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fowlpox virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTTTGTTCGTGGTGTTGGCTGGCCTACTGGGTGGGCGCAGGGATCCGGACTGAATCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTTTGTTCGTGGTGTTTGGCTGGCCTACTGGGTGGG-GTAGGGATCCGGACTGAATCCGT
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                                                                                                                                     deletions in U3, R,
been duplicated."
                                                                                                                                                                                                                                                                                                                                                                   /note="standard vaccine strain from Cyanamid-Webster Pty
Ltd, Castle Hill, New South Wales, Australia
integrated reticuloendotheliosis virus"
            DNNPVSLKTFTCPSKNSIRQFIKBLDLLRSLQSSEHVIKLYGYILDI"
                                                                                                                                                   /note="3' LTR of reticuloendotheliosis provirus; LTR has deletions in U3, R, U5 regions; first 23 bp of U3 have
                                                                                                                                                                                                 KNPSIQSPAVQATPNRDGYPRSMI"
                                                                                                                                                                                                               /translation="nrrGldLwTaEQGGICLALQEKCCFYANKSGIVRDKIRKLQEDL
IARKRALYDNPLWNGLNGFLPYLLPLLGPLFGLILFLTLGPCISKTLTRIIHAQKSGS
                                         /product="putative protein"
/protein_id="AAC58242.1"
/db_xref="GI:2393898"
                                                                                                                                                                                                                                              /codon_start=2
/product="envelope glycoprotein"
/protein_id="AACS8241.1"
/db_xref="GI:2393897"
                                                                                                                                                                                                                                                                                                                                      /gene="env"
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Fowlpox virus"
/mol_type="genomic DNA"
/strain="S (Standard Vaccine strain)"
                            translation="MDIITNTTMFDIQFNDIPNIPYVDIEKPLLVYSCDSYRLYNAKY"
                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                         gene="env"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                no RNA stage; Poxviridae; Chordopoxvirinae;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A1235533 A85 bp DNA linear Vi Fowlpox virus 'Chick-n-Pox' ORF201 gene, partial cds; Reticuloendotheliosis virus remnant LTR, complete seq protein kinase-like protein gene, partial cds.
AY255631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TGTGGGAGGGAGCTCCGGGGGAATGTGGGAGGGAGCTCCCGGGGGGAATAGCGCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 485)
Singh,P., Schnitzlein,W.M. and Tripathy,D.N.
Reticuloendotheliosis Virus Sequences Within
Strains of Fowlpox Virus Display Variability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 485)
Singh,P., Kim,T.-J. and Tripathy,D.N.
Re-emerging fowlpox: evaluation of isolates
Avian Pathol. 29, 449-455 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (13-MAR-2003) Veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fowlpox virus Viruses, no RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Illinois at Urbana-Champaign,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Singh, P., Schnitzlein, W.M. and Tripathy, D.N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                       Omaha,
                                                                                                                                                                                                                                                            Millsboro, DE vaccines for
                                                                                                                                                                                                                                                                                                                                                                                             /mol type="genomic DNA"
/strain="vaccine strain 'Chick-n-Pox'"
/db_xref="taxon:10261"
                                                                                                                                                           /note="hypothetical protein;
/codon_start=1
                                                                    protein_id="AAP21484.1"
/db_xref="GI:30267697"
                                                                                                               /evidence=not_experimental
                                                                                                                                                                                                                             /note="from Fort Dodge Animal Health, Fort Dodge, IA Indentical sequence also found in strains PP-VAC (Intervet, Inc., Millsboro, DE), Fowlpox (Mallinckrodt Veterinary, Inc., Millsboro, DE), Fowlpox (Intercontinental Biologics, Millsboro, DE), Pigeonpox (Intervet, Inc., Millsboro, DE), Pigeonpox (Intervet, Inc., Millsboro, DE), vaccines for fowlbox from Schering-Plough Animal Health, maha, NE and Select laboratories, Gainesville, GA"
'note="Reticuloendotheliosis virus
                                              translation="NNDTSLPVAVKVIYGTVTI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Fowlpox virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers,
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Pred. No. 3.3e-52;
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       remnant LTR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (30-MAY-1997) Division of Animal Health, Portarlington Road, Geelong, Victoria 3213, Austral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 2640)
Hertig.C., Coupar,B.E., Gould.A.R. and Boyle,D.B.
Field and vaccine strains of fowlpox virus carry integrated sequences from the avian retrovirus, reticuloendotheliosis virology 235 (2), 367-376 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hertig, C.H., Coupa
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Fowlpox virus M long terminal repeatinase homolog gene, complete cds,
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Fowlpox virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                  note="ORF1"
                                                                                                                                                                                                                                                                                     integrated reticuloendotheliosis virus"
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Pred. No. 4.3e-48;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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YDGTSLPVEAIHADP"
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DNNPVSLKTFTOFSKNSIRQFIKELDLLRSLQSSEHVIKLYGYLLDISVPLGSLVVEN
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NMDYGGIYNMLIKENKGEYMFLDCPLELQCIVIACRNTNSIFRPSISAIIDFLETFYS
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/note="ORF3"
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IYGTVTI"
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thes 0;
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Maximum Match 100%
Listing first 45 summaries
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6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.1	6.1	N	6.2	6.2	6.2	6.3	6.3	6.3			6.3	6.3	6.3	6.3
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Abl49336 Human pol	Adb66951 E. coli K	Abx70998 Novel hum	Aak94808 Human ful	Aad47154 Human nuc	Aak93694 Human cDN	Aak92046 Human cDN	Adb72464 Human SYK	Ada02726 Human SYK	Continuation (8 of	Aac76621 Human ORF	Abn61561 Human can	Ada71938 Rice gene	Aca92322 Lawsonia	Aai97964 Lawsonia	Ade63204 Human gen	Ade63208 Human gen	Ade63196 Human gen	Ade63200 Human gen	Ada71938 Rice gene	Abx77171 DNA seque	Adb92112 Human MDR

ALIGNMENTS

RESULT 1
AAX26109
ID AAX2
AC AAX2
AC AAX2
AC AAX2
AC AAX2
AC COLO
DT 17-Q
DT 20-W
AX VACC
AX VACC
AX VACC
AX WO99
AX WO99
AX WO99
AX O8-P
AX O 07-AUG-1998; 17-OCT-2003 20-MAY-1999 AAX26109; WPI; 1999-167428/14. Hertig 08-AUG-1997; 18-FEB-1999 Reticuloendotheliosis virus. Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV; vaccine; chicken; LTR; long terminal repeat; ss. Chicken syncytial virus provirus REV LTR sequence AAX26109 standard; DNA; 512 WO9907852-A1 (CSIR) COMMONWEALTH SCI & IND RES ORG. ú Coupar BEH, (revised)
(first entry) 97AU-00008454. 98WO-AU000628. Gould AR, BP. Boyle DB

The invention relates to a recombinant fowlpox virus (FPV) whose nucleic acid does not encode an active reticuloendotheliosis virus (REV), and whose genome does not contain any REV sequence. The recombinant FPV is used to produce a vaccine against fowlpox virus. The vaccine is used to prevent the occurrence of fowlpox virus in chickens. The chickens can be vaccinated at older than 1 day of age. Alternatively, chickens older than 1 day can be vaccinated with the vaccine subsequent to vaccination with FPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains of FPV carry integrated REV sequences. Some of the FPV strains carry a near full length provirus of REV, and can give rise to infectious REV

Example 4; Fig 5; 127pp; English.

Recombinant vaccine against fowlpox virus - is free of contamination from reticuloendotheliosis virus, used to prevent the virus occurence in

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RESULT 2
AAXX 6110
ID AAXX
XX AAXX
AC AAXX
AC AAXX
DT 20-M
XX Fowl
XX Fowl
XX Vacc
XX Fowl
XX WO95
XX WO95
XX WO95
XX O7-A
XX O8-A
XX O8-A
XX O8-A
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Best Local
                                                      07-AUG-1998;
                                                                             18-FEB-1999.
                                                                                                                                              Fowlpox virus; FPV vaccine; chicken;
         (CSIR ) COMMONWEALTH SCI & IND RES ORG
                                                                                                   WO9907852-A1
                                                                                                                           Fowlpox virus
                                                                                                                                                                              Fowlpox virus (FPV M5) LTR sequence.
                                                                                                                                                                                                       20-MAY-1999
                                                                                                                                                                                                                                                  AAX26110 standard; DNA; 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        when transfected into cell cultures and when chickens are infected. The present invention provides the means by which a FPV vaccine free from contamination by REV may be produced. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 512 BP; 130
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                                                                                                                                                                                                                                                                                                                      GGACTGAATCCGTAGTATTTCGGTACAACA 533
                                                                                                                                                                                                                                                                                                                                                               GGACTGAATCCGTAGTATTTCGGTACAACA 510
                                                                                                                                                                                                                                                                                                                                                  GTGACGTGCGGCCCCGATTCGAATCTGTAATAAAAGCTTTTTTCTTCTATATCCTCAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                           GTAAGCGGCTATATAAGCCAGGTGCATCTCTTGCTCGGGGGTCGCCGTCCTACACATTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTAAGCGGCTATATAAGCCAGGTGCATCTCTTGCTCGGGGTCGCCGTCCTACACATTGTT
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                                                                                                                                                                                                     (first entry)
                                                                                                                                           FPV; recombinant; reticuloendotheliosis en; LTR; long terminal repeat; ss.
                                                     98WO-AU000628
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                                                                                                                                                       virus;
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                                                                                                                                                         REV;
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The invention relates to a recombinant fowlpox virus (FPV) whose nucleic acid does not encode an active reticuloendotheliosis virus (REV), and whose genome does not contain any REV sequence. The recombinant FPV is used to produce a vaccine against fowlpox virus. The vaccine is used to prevent the occurrence of fowlpox virus in chickens. The chickens can be vaccinated at older than 1 day of age. Alternatively, chickens older than 1 day of age. Prior vaccine and field strains of FPV and the train at 1 day of age. Prior vaccine and field strains of FPV carry integrated REV sequences. Some of the FPV strains carry a near full length provirus of REV, and can give rise to infectious REV when transfected into cell cultures and when chickens are infected. The present invention provides the means by which a FPV vaccine free from contamination by REV may be produced. Sequences AAXX6110-115 represent FPV long terminal repeat sequences. The new recombinant FPV nucleic acid
Sequence 536 BP; 145 A; 115 C; 133 G; 143 T; 0 U; 0 Other;
                                                      molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 18; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant vaccine against fowlpox virus - is free of contamination from reticuloendotheliosis virus, used to prevent the virus occurence in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-167428/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hertig C,
                                                 can comprise a FPV LTR sequence selected from the above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coupar BEH,
                                                                                                                                                                                                                                                                                                                                                                                                                                              5; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gould AR,
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                 TGAATCCGTAGTATTTCGGTACAACA 533
                                                                      CGTGCGGCCCAGATTCGAATCTGTAATAAAAGCTTTTTTCTTCTATATCCTCAGATTGGCA
                                                                                                                     CGTGCGGCCCAGATTCGAATCTGTAATAAAAGCTTTTTCTTCTATATCCTCAGATTGGCA
                                                                                                                                                                              GCGGCTATATAAGCCAGGTGCATCTTCTTGCTCGGGGTCGCCGTCCTACACATTGTTGTGA 387
                                                 TGGTTGTAAAGGGCAGATGCTATCCTCCAATGAGGGAAAATGTCATGCAACATCCTGTAA
                                                                                                                                                                                                                                TGGTTGTAAAGGGCAGATGCTATCCTCCAATGAGGGAAAATGTCATGCAACATCCTGTAA 327
                                                                                                                                                                                                                                                                   AGACCACTTGCACCATCCAATCACGAACAAACACGAGATCGAACTATCATACTGAGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAGGGAGCTCCGGGGGGAATAGCGCTGGCTCGCTAACTGCCATATTAGCTTCTGTAATC
 TGAATCCGTAGTATTTCGGTACAACA
                                                                                                                                                            GCGGCTATATAAGCCAGGTGCATCTCTTGCTCGGGGTCGCCGTCCTACACATTGTTGTGA
                                                                                                                                                                                                                                                                                       AGACCACTTGCACCATCCAATCACGAACAAACACGAGATCGAACTATCATACTGAGCCAA 267
                                                                                                                                                                                                                                                                                                                         ATGCTTGCCTTAGCCGCCATTGTACTTGATATTTCGCTGATATCATTTCTCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                               GGAGGGAGCTCCGGGGAATAGCGCTGGCTAACTGCCATATTAGCTTCTGTAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.9%; Score 506; DB 2; L, 100.0%; Pred. No. 1.7e-161; tive 0; Mismatches 0;
534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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RESULT 3
AAX26113
ID AAX2
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AAX26113

standard; DNA; 4643

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AAX26113;

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Query Match
Best Local Sim.
Matches 506;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CC The invention relates to a recombinant fowlpox virus (FPV) whose nucleic CC acid does not encode an active reticuloendotheliosis virus (REV), and CC whose genome does not contain any REV sequence. The recombinant FPV is CC used to produce a vaccine against fowlpox virus. The vaccine is used to prevent the occurrence of fowlpox virus in chickens. The chickens can be CC vaccinated at older than 1 day of age. Alternatively, chickens older than 1 day of age. Prior vaccine and field strains CC 1 day can be vaccinated with the vaccine subsequent to vaccination with CC pPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains CC of FPV carry integrated REV sequences. Some of the FPV strains carry a near full length provirus of REV, and can give rise to infectious REV CC when transfected into cell cultures and when chickens are infected. The CC present invention provides the means by which a FPV vaccine free from CC contamination by REV may be produced. Sequences AXX56110-115 represent CC FPV long terminal repeat sequences. The new recombinant FPV nucleic acid molecule can comprise a FPV LTR sequence selected from the above
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4643 BP; 1326 A; 1015 C; 1127 G; 1175 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 18; Fig 6; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant vaccine against fowlpox virus - is free of contamination reticuloendotheliosis virus, used to prevent the virus occurence in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV, vaccine; chicken; LTR; long terminal repeat; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-167428/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hertig C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fowlpox virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fowlpox virus (FPV S) 5' LTR sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CSIR ) COMMONWEALTH SCI & IND RES ORG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-1999.
                                                                                                                                                                                                                                                                            1259
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                                                                                                                                                                    148
                                                                                                                                                                                                                             88 ATGCTTGCCTTAGCCGCCATTGTACTTGATATATTTCGCTGATATCATTTCTCGGA
                                                                                                                                                                                                                                                                                                            28 GGAGGGAGCTCCGGGGGAATAGCGCTGGCTCGCTAACTGCCATATTAGCTTCTGTAATC
                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                          ATGCTTGCCTTAGCCGCCATTGTACTTGATATATTTCGCTGATATCATTTCTCGGA
                                                                                                                                                                                                                                                                            GGAGGGAGCTCCGGGGGGAATAGCGCTGGCTCGCTAACTGCCATATTAGCTTCTGTAATC
                            TGGTTGTAAAGGGCAGATGCTATCCTCCAATGAGGGAAAATGTCATGCAACATCCTGTAA
                                                                                                   AGACCACTTGCACCATCCAATCACGAACAACACGAGATCGAACTATCATACTGAGCCAA
                                                                                                                                    Coupar BEH,
                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                             94.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gould AR, Boyle
                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                             Score 506; DB 2; L; Pred. No. 5.2e-161;
                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                               <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                              Length 4643;
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                                                                                                                                                                                                                                                                                                                                               Gaps
1558
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GTAATCATGCTTGCCTTAGCCGCCATTGTACTTGATATATTTCGCTGAT----AAUGUGGGAGGGAGCUCCGGGGGGAAUAGCGCUGGCUAACUGCCAUAUUAGCUUCU **AATGTGGGAGGGAGCTCCGGGGGGAATAGCGCTGGCTCGCTAACTGCCATATTAGCTTCT**

134 60 81 Matches

Conservative 135; Mismatches

Indels Length 940;

25;

Gaps

82.4%;

Score 439.4; DB 2; Pred. No. 1.1e-138;

22

Query Match Best Local Similarity

Sequence 940 BP; 190 A; 225 C; 260 G; 0 T; 265 U; 0 Other;

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ARSSULT 4
ARVS3778
ID 3AV6
XX AAV6
XX AAV6
XX AAV6
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XX Reti
XX Reti
XX Reti
XX FET
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                                                   The present sequence is derived from the 5' end of the genomic RNA of Reticuloendotheliosis virus type A (REV-A). The specification also describes nuclectide sequence derived from all or part of the 5' end of the genomic RNA of a type C retrovirus other than Friend murine leukaemia virus (FMLV) and Moloney murine leukaemia virus (MoMLV). The 5' derived sequences are used as an internal ribbsome entry site (IRES) in a vector for permitting or enhancing the encapsidation of a retroviral vector. The vectors can be used for gene therapy, production of recombinant polypeptides or production of transgenic animals
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 31-32; 43pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expression vectors containing IRES and/or encapsidation enhancer derived from type C retrovirus other than FMLV and MoMLV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reticuloendotheliosis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type C retrovirus; internal ribosome retroviral vector; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reticuloendotheliosis virus type A; REV-A; 5' end genomic RNA; type C retrovirus; internal ribosome entry site; IRES; encapsi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lopez Lastra M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INRM ) INSERM INST NAT SANTE & RECH MEDICALE
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The invention relates to a recombinant fowlpox virus (FPV) whose nucleic acid does not encode an active reticuloendotheliosis virus (REV), and whose genome does not contain any REV sequence. The recombinant FPV is used to produce a vaccine against fowlpox virus. The vaccine is used to prevent the occurrence of fowlpox virus in chickens. The chickens can be vaccinated at older than 1 day of age. Alternatively, chickens older than
                                                                                                                                   Claim 18;
                                                                                                                                                                        Recombinant vaccine against fowlpox virus - i reticuloendotheliosis virus, used to prevent
                                                                                                                                                                                                                                                                 Hertig C,
                                                                                                                                                                                                                                                                                                                                08-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                               07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fowlpox virus; FPV; vaccine; chicken; L7
                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fowlpox virus
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                                                                                                                                                                                                                                1999-167428/14
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                                                                                                                                                                                                                                                             Coupar BEH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FPV S3') LTR sequence.
                                                                                                                                                                                                                                                                                                                           97AU-00008454.
                                                                                                                                                                                                                                                                                                                                                            98WO-AU000628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant; reticuloendoTR; long terminal repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
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                                                                                                                                                                                                                                                            AR,
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                                                                                                                                                                                                                                                          Boyle
                                                                                                                                                                                                                                                          DB
                                                                                                                                                                 is free of contamination the virus occurence in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                      chickens.
                                                                                               Recombinant vaccine acreticuloendotheliosis
                                                                                                                                                      Hertig
                                                                                                                               WPI; 1999-167428/14.
                                                                                                                                                                                                 08-AUG-1997;
                                                                                                                                                                                                                      07-AUG-1998;
                                                                                                                                                                                                                                              18-FEB-1999,
                                                                                                                                                                                                                                                                  WO9907852-A1
                                                                                                                                                                                                                                                                                                            Fowlpox virus; FPV; rec
vaccine; chicken; LTR;
                                                                                                                                                                                                                                                                                                                                          Fowlpox virus (FPV S) 3' LTR sequence.
                                                                                                                                                                                                                                                                                        Fowlpox virus.
                                                                                                                                                                                                                                                                                                                                                                      20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                            AAX26115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 day can be vaccinated with the vaccine subsequent to vaccination with FPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains of FPV carry integrated REV sequences. Some of the FPV strains carry a near full length provirus of REV, and can give rise to infectious REV when transfected into cell cultures and when chickens are infected. The contamination by REV may be produced. Sequences AAX26110-115 represent FPV long terminal repeat sequences. The new recombinant FPV nucleic acid molecule can comprise a FPV LTR sequence selected from the above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                       COMMONWEALTH SCI & IND RES
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                                                                                                                                                                                                                                                                                                                                                                                                              standard; DNA; 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGAAATGTTTGTTGAAGGCAAGCATCAGACCACTTGCAC 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAAAATGTTTGTTGAAGGCAAGCATCAGACCACTTGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATATTTCGCTGATATCATTTCTCGGAATCGGCATCAAGAGCAGGCTCATAAACCATAAA
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                                                                                                                                                   Coupar BEH,
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                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                               97AU-00008454.
                                                                                                                                                                                                                    98WO-AU000628.
                                                                                            e against f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 A; 58 C; 81 G; 82 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                       recombinant; reticuloendotheliosis TR; long terminal repeat; ss.
                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.7%;
99.1%;
                                                                                                                                                   Gould
                                                                                      fowlpox virus - is free of contamination, used to prevent the virus occurence in
                                                                                                                                                  AR,
                                                                                                                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 206.4; DB
Pred. No. 1.5e-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                         ORG.
                                                                                                                                                  Boyle
                                                                                                                                                 DB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .5e-59;
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                                                                                                                                                                                                                                                                                                                 virus;
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The invention relates to a recombinant fowlpox virus (FPV) whose nucleic acid does not encode an active reticuloendotheliosis virus (REV), and whose genome does not contain any REV sequence. The recombinant FPV is used to produce a vaccine against fowlpox virus. The vaccine is used to prevent the occurrence of fowlpox virus in chickens. The chickens can be

Claim 18; Fig

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127pp; English.

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Query Match
Best Local Similarity 99.1
Conservative
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                                                                                                                                   Recombinant vaccine against fowlpox virus - is free of contamination reticuloendotheliosis virus, used to prevent the virus occurence in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV; vaccine; chicken; LTR; long terminal repeat; ss.
                                                                                                                                                                                       WPI; 1999-167428/14.
                                                                                                                                                                                                                         Hertig
                                                                                                                                                                                                                                                                                                                             07-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Fowlpox virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fowlpox virus (FPV M3) LTR sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX26112;
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                                                                                                                                                                                                                                                         (CSIR ) COMMONWEALTH SCI & IND RES
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                                                                                                                                                                                                                         Coupar BEH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                           97AU-00008454.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
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Pred. No. 2.9e-59;
                                                                                                                                                                                                                                                             ORG.
                                                                                                                                                                                                                         Boyle DB
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The invention relates to a recombinant fowlpox virus (FPV) whose nucleic acid does not encode an active reticuloendotheliosis virus (REV), and whose genome does not contain any REV sequence. The recombinant FPV is used to produce a vaccine against fowlpox virus. The vaccine is used to

The invention relates to a recombinant fowlpox virus (FPV) whose nucleic acid does not encode an active reticuloendotheliosis virus (REV), and whose genome does not contain any REV sequence. The recombinant FPV is

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127pp; English.

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                                                                                                                                                                                        Recombinant vaccine against fowlpox virus - is free of reticuloendotheliosis virus, used to prevent the virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fowlpox virus; vaccine; chicke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fowlpox virus (FPV M3) LTR sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX26114 standard; DNA; 1100
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                                                                                                         Claim 18; Fig 6; 127pp; English.
                                                                                                                                                                                                                                                                          WPI; 1999-167428/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                       08-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chicken;
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                                                                                                                                                                                                                                                                                                                                Coupar BEH,
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Pred. No. 5.5e-55;
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                                                                                                                                                                                                                                                                                                                                Boyle
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                                                                                                                                                                                           contamination from occurence in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 virus;
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Treating and/or preventing e.g. malaria or tuberculosis, or eliciting an immune response, comprises administering a priming composition and a boosting composition containing a non-replicating viral vector in either
                                                                                                                                               30-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                    WPI; 2003-513700/48.
                                                                                                                                                                                  02-DEC-2002; 2002WO-GB005411
                                                                                                                                                                                                                                                                           fowlpox virus; FPV; virucide; tuberculostatic; protozoacide; antipyretic; cytostatic; hepatotropic; antibacterial; vaccine; malaria; tuberculosis; East Coast fever; aripox virus; influenza; hepatitis; human papilloma virus; tumour; leishmaniasis; listeriosis; theileria; gene; ds.
                                                                                                                                                                                                                 12-JUN-2003.
                                                                                                                                                                                                                                        WO2003047617-A2
                                                                                                                                                                                                                                                                Fowlpox virus.
                                                                                                                                                                                                                                                                                                                                                                Fowlpox virus genome DNA.
                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADE87477 standard; DNA; 266145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used to produce a vaccine against fowlpox virus. The vaccine is used to prevent the occurrence of fowlpox virus in chickens. The chickens can be vaccinated at older than 1 day of age. Alternatively, chickens clear than 1 day of age and to vaccinated with the vaccine subsequent to vaccination with of FPV mild strain) at 1 day of age. Prior vaccine and field strains of FPV carry integrated REV sequences. Some of the FPV strains carry a when transfected into cell cultures and when chickens are infected. The present invention provides the means by which a FPV vaccine free from FPV long terminal repeat sequences. The new recombinant FPV nucleic acid molecule can comprise a FPV LTR sequence selected from the above
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                                                                                                                 ISIS INNOVATION LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGACCACTTGCAC 220
                                                                                           Skinner M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGGGAGCTCCGGGGGAATAGCGCTGGCTCGCTAACTGCCATATTAGCTTCTGTAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1100 BP; 392 A; 177 C; 196 G; 335 T; 0 U; 0 Other;
                                                                                                                                            2001GB-00028733.
2001US-0334649P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.2%; 5
100.0%; Pr
                                                                                        Hill A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 193; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
                                                                                      Gilbert S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                    Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
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RESULT 10
AV63779
ID AAV63779
XX AV63
XX AV63
XX AV63
XX 17-MA
XX Seque
XX Retic
XX Fetro
XX Fetro
XX Fetro
XX Ferro
XX Ferro
XX Ferro
PN 90-OC
XX 28-AP
XX 28-AP
XX 1NRM
PA (INRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC The invention relates to a fowlpox virus (FPV) genome which has CC modifications in one or more wild-type FPV genes. The invention further CC subject comprising administering two compositions, each containing a non-CC explicating viral vector. At least one of the compositions comprises a CC poxvirus vector derived from a fowlpox virus. The novel compositions have CC poxvirus vector derived from a fowlpox virus. The novel compositions have CC complete the following activities: virucide, tuberculostatic, protozoacide, complicating viral vector is useful in a vaccine for an animal. The non-CC particularly a mammal such as a primate, specifically human. The priming composition, or the kit is useful for manufacturing a CC from, a chronic infection such as malaria, tuberculosis or East Coast CC cultured CEF cells are useful for growing an avinox virus, such as CC cultured CEF cells are useful for growing an avipox virus, such as CC prevent influenza, hepatitis, human papilloma virus and other viral compositions, malignancies such as tumours, leishmaniasis, listeriosis, and CC virus genome of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local 9
   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                      28-APR-1997;
                                                                                                                                                                  Reticuloendotheliosis virus type A; REV-A; type C retrovirus; internal ribosome entry retroviral vector; gene therapy; ss.
                                                                 28-APR-1997;
                                                                                                                                               Reticuloendotheliosis virus
                                                                                              30-OCT-1998
                                                                                                                         FR2762615-A1
                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                  17-MAR-1999
                                                                                                                                                                                                                                                                                              AAV63779;
                                                                                                                                                                                                                                                                                                                   AAV63779 standard; DNA; 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 266145 BP; 92375 A; 41026 C; 40846 G; 91897 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                               221921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 30; SEQ ID NO 1; 302pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
                                                                                                                                                                                                                            derived from the 5' end of REV-A.
                                                                                                                                                                                                                                                                                                                                                                                                        AGACCACTTGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGCTTGCTTGCCTTAGCCGCCATTGTACTTGATATATTTCGCTGATATCATTTCTCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAGGGAGCTCCGGGGGGAATAGCGCTGGCTCGCTAACTGCCATATTAGCTTCTGTAATC
                                                                                                                                                                                                                                                           (first entry)
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                                   97FR-00005203
                                                              97FR-00005203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.2%; Score 193; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                   220
                                                                                                                                                                                                                                                                                                                     ₽₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2e-53;
                                                                                                                                                                            5' end genomic RNA;
site; IRES; encapsidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 266145;
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Lopez Lastra

Σ,

Gabus

Darlix

Darlix

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RESULT 11
AAQ76041
ID AAQ76
XX AQ76
XX AQ76
XX AQ76
XX AQ76
XX Retro
DE Retro
XX Retro
CX Splee
XX W0942
XX W0942
XX W0942
XX W07-JU
XX QT-JU
XX QT-JU
XX QT-JU
XX QT-JU
XX QT-JU
XX QT-JU
XX AQ76
PR QT-JU
XX QT-JU
XX AQ76
PR QT-JU
XX AQ76
PT COOTH
XX AQ76
PT Recort
PT FOrm
XX Examp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is derived from the 5' end of the genomic RNA of Reticuloendotheliosis virus type A (REV-A). The specification also describes nucleotide sequence derived from all or part of the 5' end of the genomic RNA of a type C retrovirus other than Friend murine leukaemia virus (FMLV) and Moloney murine leukaemia virus (MoMLV). The 5' derived sequences are used as an internal ribosome entry site (IRSS) in a vector for permitting or enhancing the encapsidation of a retroviral vector. The vectors can be used for gene therapy, production of recombinant
                                                    Recombinant retrovirus vector, contg. non-retroviral gene, - ha
                                                                                                                                                                                                                                                           07-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                         Spleen necrosis virus.
                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
20-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ76041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ76041 standard; DNA; 3878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 578 BP; 94 A; 139 C; 172 G; 0 T; 173 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                              WPI; 1995-036467/05.
                                                                                                                                                                                                                                                                                                 22-DEC-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                               Retrovirus; vector; pPO115-R1; spleen necrosis virus; SNV; gene transfer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptides or production of transgenic animals
                                                                                                                                                Dornburg RC
                                                                                                                                                                                     (UYNE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 GGGGTCGCCGTCCTACACATTGTTGTGACGTGCGGCCCAGATTCGAATCTGTAATAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Page 32; 43pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ion vectors containing IRES and/or encapsidation enhancer from type C retrovirus other than FMLV and MoMLV.
                                                                                                                                                                                     VIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UUUUUUUUCUUCUAUAUCCUCAGAUUGGCAGUGAGAGGAGAUUUUGUUCGUGGUGUAGGCU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCCUACUGGGUGGGGUAGGGGUCCGGACUGAAUCCGUAGUAUUUCGAUACAACA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCCTACTGGGTGGGGTAGGGATCCGGACTGAATCCGTAGTATTTCGGTACAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -CTTTTTCTTCTATATCCTCAGATTGGCAGTGAGAGGAGATTTTGTTCGTGGTGTTTGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                vector pPO115-R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                     NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                                                                                                                                                          93US-00073345
                                                                                                                                                                                                                                                             94WO-US006415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 155; DB 2
Pred. No. 7e-42;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>υ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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δ 밁 δ 밁 Ś

Example; Page 17;

28pp; English

New recombination-free, highly efficient retroviral vectors pPO111-R1 (given in AAQ76038), pPO111-R2 (AAQ76039) and pPO111-R3 (AAQ76040) wer obtained by replacing the U3 region of the left LTR of spleen necrosis virus with the IE promoter/enhancer of CMV, and extension of the

Page

13-14;

28pp; English

provirus.

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ARGSULT 12
ARACT6038
ID 76038
ID 76038
ID 76038
AC AAQ76
XX AAQ76
XX AAQ76
XX Petro
XX Retro
XX Retro
XX Retro
XX Splee
XX Splee
XX Splee
XX CYtom
XX O7-JU

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 189;
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                                                                                                                                                                                                       Recombinant retrovirus vector, contg. non-retroviral gene, - has ability to produce progeny virus, in helper cell which can infect host cell and
                                                                                                                                                                                                                                                                                     WPI; 1995-036467/05
                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spleen necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Retrovirus; vector; pPO111-R1; spleen necrosis virus; SNV; cytomegalovirus; CMV; intermediate-early promoter; IE prom long terminal repeat; LTR; encapsidation; gene transfer; g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Retrovirus
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20-JUL-1995
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                                                                                                                                                                                                                                                                                                                                   Dornburg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-DEC-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9429437-A1.
                                                                                                                                                                                                                                                                                                                                                                                           (UYNE-) UNIV
                                                                                                                                                                            roduce progeny provirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACGTGCGGCCCAGATTCGAATCTGTAATAAAA-GCTTTTTTCTTCTATATCCTCAGATTGG
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(first entry)
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Pred. No. 4.9e-38;
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gene transfer; gene therapy;
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Best Local Sim
Matches 189;
    New recombination-free, highly efficient retroviral vectors pp0111-R1 (given in AAQ76038), pp0111-R2 (AAQ76039) and pp0111-R3 (AAQ76040) were obtained by replacing the U3 region of the left LTR of spleen necrosis virus with the IE promoter/enhancer of CMV, and extension of the encapsidation region. The vectors allow cell-type specific gene expression and eliminate risks of downstream activation of cellular proto-concogenes. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                               Example; Page 14-16; 28pp; English.
                                                                                                                                                                                                                                                                 Recombinant retrovirus vector, contg
                                                                                                                                                                                                                                                                                                                                            WPI; 1995-036467/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Retrovirus; vector; pPO111-R2; spleen necrosis virus; SNV; cytomegalovirus; CNV; intermediate-early promoter; IE promoter; compater; com
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elper cell which can infect host
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Pred. No. 5.
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RESULT 14
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Best Local :
                       New recombination-free, highly efficient retroviral vectors pp0111-R1 (given in AAQ76038), pp0111-R2 (AAQ76039) and pp0111-R3 (AAQ76040) were obtained by replacing the U3 region of the left LTR of spleen necrosis virus with the IE promoter/enhancer of CMV, and extension of the encapsidation region. The vectors allow cell-type specific gene expression and eliminate risks of downstream activation of cellular proto-oncogenes. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                             Example; Page 16-17; 28pp; English.
                                                                                                                                                                                                                                                                    form provirus.
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milarity 92.6%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rmediate-early promoter; IE promoter, encapsidation, gene transfer; gene t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
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Pred. No. 2e
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st cell and
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Query Match Best Local Similarity

23.9%;

Score 127.6; DB Pred. No. 5e-32;

2

Sequence

5519

ВP;

1264 A; 1420 C; 1456 G;

1379 Т;

0 U; 0 Other;

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AAK91988 standard; cDNA; 714 BP.
XX
AC AAK91988 standard; cDNA; 714 BP.
XX
AC AAK91988;
XX

AX 06-NOV-2001 (first entry)
DT 06-NOV-2001 (first entry)
DE Human cDNA 5'-end sequence, SEQ ID
XX
Human cDNA 5'-end sequence, SEQ ID
XX
Homo sapiens.
XX

PD 05-SEP-2001.
XX

OS Homo sapiens.
XX

OS-JUL-1999; 99JP-00114089.
XX

O8-JUL-1999; 99JP-00119774.
PR 02-MAY-2000; 2000JP-00118774.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183765.
XX

OCA T, Nishikawa T, Isogai T, H
PI Wakamatsu A, Suglyama T, Nagai K
XX

PA (HELI-) HELIX RES INST.
XX

PA (HELI-) HELIX RES INST.
XX

CO That T, Nishikawa T, Isogai T, H
PI Wakamatsu A, Suglyama T, Nagai K
XX

PA (HELI-) HELIX RES INST.
XX

CO The invention for synthesizin in genetic manipulation.
XX

Claim 2; SEQ ID NO 448; 1380pp + S
XX

Claim 2; SEQ ID NO 448; 1380pp + S
CC clones. 830 CDNA molecules encodir and nucleotide sequences of 5'- ar colones. 830 CDNA molecules of 5'- ar colones. 830 CDNA molecules of 5'- are been determined. Primers for synthesized by centrode. The present sequence is to been determined. Primers for synthesised by centrode. The production of the full methods. The present sequence is to a cDNA provided in the invention. CC add not form part of the printed (CC add not form part o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
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         Query Match 6.3
Best Local Similarity 54.4
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; SEQ ID NO 448; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; full length cDNA; cDNA synthesis; oligo-capping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA 5'-end sequence, SEQ ID NO: 448.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            732 TANAACTTTTTTTTTTTCTGAATCCTCAGATTGGCAGTGAGAGGAGATTTTGTTCGTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nishikawa T, Isogai T, Hayashi K,
su A, Sugiyama T, Nagai K, Kojima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA 853
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                                     6.3%;
                                                                                                                                 A; 215 C; 193 G; 167 T; 0 U; 3 Other;
Score 33.8; DB 4;
Pred. No. 1.6;
0; Mismatches 57;
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a S, Otsuki
            57; Indels
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                                                                  Length 714;
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T, Koga H;
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                      514 CGTAG 518
                                                                   TGAGATGTGTCTTCTTTAGCCTCCTCAGGGGCAGAGGCTAGGGACGGGGACAGGGC 411
                                                                                              GTCAAAATTCCCATCAGTTACAAAAGCTAAATTCTCTAGATCAGCAAGCTGCCTTTGAAT 471
                                                                                                                   GCCCAGATTCGAATCTGTAATAAAAGCTTTTTCTTCTATATCCTCAGATTGGCAGTGAGA 453
CGGAG 406
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Search completed: May 25, 2004, 02:15:46 Job time: 355 secs

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Run

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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2
2: /cgn2_6/ptodata/2
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length: 2000000000
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Match Length DB
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533
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  Copyright
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              4 US-08-916-4218-1
US-08-96-176-36
US-08-96-176-31
US-08-9453-7028-111
US-09-453-7028-111
US-09-453-7028-11
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US-09-410-644-77
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US-09-411-5
US-09-411-5
US-09-335-411-5
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3399.872 Million cell updates/sec
              Sequence 1, Appli
Sequence 36, Appli
Sequence 36, Appli
Sequence 11, Appli
Sequence 111, Appli
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Sequence 113, Ap
Sequence 114, Appli
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Sequence 17, Appli
Sequence 77, Appli
Sequence 145, Appli
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Sequence 5, Appli
Sequence 55, Appli
Sequence 55, Appli
Sequence 31, Appli
Sequence 348, App
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US-09-689-065B-1/c

Sequence 1, Application US/09689065B.

Sequence 1, Application US/09689065B.

Sequence 1, Application US/09689065B.

Patent NO. 6605596

GENERAL INFORMATION:

APPLICANT: Pfizer Products, Inc.

PITLE OF INVENTION: MATERIALS

FILE REFERENCE: 3153.00187/PC10589A

CURRENT APPLICATION NUMBER: US/09/689,065B

CURRENT EILING DATE: 2000-10-12

PRIOR APPLICATION NUMBER: US Prov. 60/160,922

PRIOR FILING DATE: 1999-10-22

PRIOR APPLICATION NUMBER: US Prov. 60/163,858

PRIOR FILING DATE: 1999-11-05

PRIOR FILING DATE: 1999-11-05
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NUMBER OF SEQ ID NOS: 112 SOFTWARE: PatentIn version SEQ ID NO 1 LENGTH: 6617

version 3.2

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29 29.6 5.6 783 4 US-09-107-532A-2943 30 29.4 5.5 2141 4 US-09-841-786-11 31 29.4 5.5 4545 6 5183884-3 32 29.4 5.5 4905 1 US-07-978 895-3 33 29.4 5.5 4905 1 US-08-473-119-3 34 29.4 5.5 4905 2 US-08-473-119-3 35 29.4 5.5 4905 2 US-09-170-699-3 36 29.4 5.5 4905 3 US-09-170-699-3 37 29.4 5.5 4972 3 US-09-035-648-17 38 29.4 5.5 4972 3 US-09-01-951-17 38 29.4 5.5 4972 3 US-09-01-951-17 38 29.4 5.5 4972 3 US-09-630-706-3 40 29.4 5.5 4972 3 US-09-841-786-8 41 29.4 5.5 9726 4 US-09-841-786-18 41 29.4 5.5 11130 4 US-09-841-786-15 42 29.4 5.5 392000 4 US-09-841-786-15 43 29.2 5.5 89047 4 US-09-540-236-1230 44 29.2 5.5 89047 4 US-09-540-236-1230	29.6 5.6 783 4 29.4 5.5 4905 1 29.4 5.5 4905 1 29.4 5.5 4905 1 29.4 5.5 4905 2 29.4 5.5 4972 3 29.4 5.5 4972 3 29.4 5.5 4972 3 29.4 5.5 4972 3 29.4 5.5 4972 3 29.4 5.5 4972 3 29.4 5.5 4972 3 29.4 5.5 4972 3 29.4 5.5 4972 3 29.4 5.5 4972 3 29.4 5.5 4972 3 29.4 5.5 4972 3 29.4 5.5 4972 3 29.4 5.5 4972 3 29.4 5.5 4972 3 29.4 5.5 4972 3 29.4 5.5 4972 3 29.4 5.5 4972 3 29.4 5.5 4972 3 29.4 5.5 4973 3 29.4 5.5 4973 3 29.4 5.5 4973 3 29.4 5.5 4973 3 29.4 5.5 4973 3 29.4 5.5 4973 3 29.4 5.5 4973 3 29.4 5.5 4973 3 29.4 5.5 4973 3 29.4 5.5 4973 3 29.4 5.5 4973 3 20.4 20.4 20.4 20.4 20.4 20.4 20.4 20.4	Ω	ი	ი	ი	Ω	ი	O	ი	ი	ი	ი	ი	ი	ი	ი	ი	ი	
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4 US-09-107-532A-2943 4 US-09-841-786-11 6 5183884-3 1 US-07-978-895-3 1 US-08-473-119-3 1 US-08-475-352-3 4 US-09-170-699-3 2 US-09-035-648-17 3 US-09-035-648-17 3 US-09-035-648-17 3 US-09-035-648-17 4 US-09-818-829-17 4 US-09-841-786-8 4 US-09-841-786-15 4 US-09-841-786-15 4 US-09-841-786-15 4 US-09-841-786-15 4 US-09-541-236-1230 4 US-09-540-236-1230 4 US-09-543-681A-2518	3 Sequence Sequence Patent No. Sequence	2184	89047	2079	392000	11130	9726	4975	4972	4972	4972	4905	4905	4905	4905	4545	2141	783	
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ALIGNMENTS

AND

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RESULT 2
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            Sequence 1, Application US/08916421B
Patent No. 6503729
GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence
Patent No. 6503729
TITLE OF INVENTION: jannaschii
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Best Local Similarity
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FILE REFERENCE: PB275
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                                                                                                                                                                                                                                  346
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                                                                                                                                                                                                   ACCTTCCCCTGCTGCTGGCATTCC 1629
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                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                of the Methanogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 6617;
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SEQ ID NO 1 NAME/KEY: misc feature
LOCATION: (84773) .. (84773)
OTHER INFORMATION: n equals a
OTHER INFORMATION: n cquals a CURRENT APPLICATION NUMBER: US/08/916,421B CURRENT FILING DATE: 1997-08-22 PRIOR APPLICATION NUMBER: US 60/024,428 PRIOR FILING DATE: 1996-08-22 NUMBER OF SEQ ID NOS: 3 OTHER INFORMAT: NAME/KEY: misc_ NAME/KEY: misc feature LOCATION: (103998)..(103998) OTHER INFORMATION: n equals SOFTWARE: PatentIn version 3.1 OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (191995)..(191995) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (148948)..(148948) OTHER INFORMATION: n equals NAME/KEY: misc NAME/KEY: misc feature LOCATION: (163385)...(163385) OTHER INFORMATION: n equals LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals NAME/KEY: misc facture (98239) OTHER INFORMATION: n emisi AME/KEY: misc NAME/KEY: misc THER INFORMATION: n equals IAME/KEY: misc OTHER INFORMATION: n equals LOCATION: (84808)..(84808)

OTHER INFORMATION: n equals LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals ORGANISM: Methanococcus jannaschii OTHER INFORMATION: n ENGTH: INFORMATION: n equals a, KEY: misc_feature ION: (234220)..(234220) INFORMATION: n equals a, ION: (234187)..(234187) INFORMATION: n equals a, ION: (98266)..(98266)
INFORMATION: n equals INFORMATION: n emisl 1664976 (191989) . . (191989) (231980).. (84808) . . (84808) 281 teature teature reature feature reature reature feature n equals (84812) (231980) (28222) equals equals D) a a, a, a, e, 'n, D) a, a, ā a, , ŗ ŗ ζ† ŗ ŗ Ç ū ۲, ή, ŗ , Ļ ŗ Ĺ ŗ ŗ ŗ ņ Ç ņ ņ ņ ç ů 'n ú ū ú ç ú ů Ç ç ņ ņ ó ç ö or ç ö õ or 유 or or 9 õ õ or õ ဝူ ω ιO ω ω ω ω ιQ g g ω ω Ω g ω

NAME/KEY: misc_feature
LOCATION: (85539). (85539)
OTHER INFORWATION: n equals a
NAME/KEY: misc_feature
LOCATION: (871619). (871619)
OTHER INFORWATION: n equals a
NAME/KEY: misc_feature OTHER INFORMATION: (1310988)...(1310988) LOCATION: (1119881)....
LOCATION: (1119881)...
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
'COCATION: (1130881)...
'TOCATION: (1130881)...
'TOCATION: (1130881)... NAME/KEY: misc feature LOCATION: (1349473)..(: OTHER INFORMATION: (1096846)..(1096846)
NAME/KEY: misc_feature OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (1313224)..(1313224) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (1096846)..(109684 NAME/KEY: misc feature LOCATION: (779676)...(779676) OTHER INFORMATION: n equals JOCATION: (1130881)..(113088 NAME/KEY: misc feature LOCATION: (779455)...(779455) OTHER INFORMATION: n equals NAME/KEY: misc teature LOCATION: (741684)..(741684) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (713652)..(713652) COTHER INFORMATION: n equals a, OCATION: LOCATION: (674435)...(674435)
OTHER INFORMATION: n equals
NAMS/KEY: misc feature
LOCATION: (682442)...(682442)
OTHER INFORMATION: n equals LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals
NAME/KEY: misc feature NAME/KEY: misc_feature INCATION: (657081)..(657081) NAME/KEY: misc feature LOCATION: (622708)..(622708) OTHER INFORMATION: n equals OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (312837)...(312837) OTHER INFORMATION: n equals a, LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals
NAME/KEY: misc_feature LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals COCATION: (600992)..(600992) OTHER INFORMATION: n equals NAME/KEY: misc_ NAME/KEY: misc OTHER INFORMATION: n equals (1084830)..(1084830))RMATION: n equals a, feature reature eature .(1349473) equals a, (559241) (559167)(312993) à à a, a a a a a, a) Ω, ā a a, a a, ή, ζ, ŗ , ŗ ŗ ŗ ŗ ŗ Ţ ŗ Ĺ ŗ ŗ Ĺ ,, Ţ ŗ ŗ ŗ ç ņ ú Ç 'n ú ú ú ç ņ ū ç ņ ú ú Ç ņ ú ņ ņ ú õ ņ ç õ õ õ 유 ö õ 9 õ e õ õ or Or. or R 6 õ ဝူ ę ဝူ 0 F õ ů, ဝူ 얹 얹 ω ω ω g Q ω ω ω ω ıΩ ω g ω g ω

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                                       US-10-204-708-36
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                                                                                                                                                                                              PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR PELICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
                                                                                                                                     NUMBER OF SEQ ID NOS: 98
SEQ ID NO 36
LENGTH: 9347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36, Application US/10204708
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Best Local Similarity
Query Match
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                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OLEK, Alexander
APPLICANT: PIEDENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENERAL INFORMATION:
                                                                             ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (1664854)..(1664855)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature LOCATION: (1602912)...(1602912) OTHER INFORMATION: n equals a,
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LOCATION: (1569020)..(1569020)
OTHER INFORMATION: n equals a,
                                                                                                                       TYPE: DNA
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LOCATION: (1603734)..(1603734)
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LOCATION: (1470091)..(1470091)
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OTHER INFORMATION: n equals a,
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LOCATION: (1349491)..(1349491)
                                                          OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: n equals a,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 AACACGAGATCGAACTATCATACTGAGCCAATGGTTGTAAAGGGCAGATGCTATCCTCCA 296
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  6.0%;
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Pred. No. 26;
Score 32;
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Length 9347;
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                                                                                                                                                                                                                                                                  TELEPHONE: 206-547-80: TELEFAX: 206-548-2329 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
PEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: PARKEY, GARY E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 8878 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Foster, Donald C
TITLE OF INVENTION: Product:
TITLE OF INVENTION: Animals
                                                            FEATURE:
NAME/KEY:
                                                                                                                          FEATURE:
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CORRESPONDENCE ADDRESS:
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                                                                                          NAME/KBY:
LOCATION:
                                                                                                                                       CLONE:
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/206,176 FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                             LOCATION:
                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                              LENGTH: 8878 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 TACTGAGCCAATGGTTGTAAAGGGCAGATGCTATCCTCCAATGAGGGAAAATGTCATGCA 316
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3: WA
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4225 Roosevelt Way, N.E.
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Prunkard, Donna
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470..583
intron
584..3257
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; Sequence 1, Application US/08943731
Patent No. 6265157
; GENERAL INFORMATION:
APPLICANT: PROCKOP, DARWIN J.
APPLICANT: SPOTILA, LORETTA D.
APPLICANT: DELTAS, CONSTANTINOS D
APPLICANT: SEREDA, LARISA
                                                                         RESULT 5
US-08-943-731-1
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; LOCATION:
US-08-206-176-3
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Matches
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Best Local Similarity
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FEATURE:
NAME/KEY:
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NAME/KEY:
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NAME/KEY:
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LOCATION:
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LOCATION:
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LOCATION:
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                                                                                                                                    144 СССАЛТССССАТСАЛСАСЛССТСАТАЛАССАТАЛА 180
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                                                                                                               TATAATTTTATAAATAGTAATCTCAGTAACAATATA 1013
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 PROCKOP, DARWIN J.
SPOTILLA, LORETTA D.
DELTAS, CONSTANTINOS D.
SEREDA, LARISA
                                                                                                                                                                                                    5.9%; Score 31.4; llarity 57.7%; Pred. No. 3. Conservative 0; Mismatche
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8538..8878
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8103..8537
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7871..8102
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5831..5944, 6633..6758, 6967..7252, 7871..8102)
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6759..6966
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5945..6632
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6967..7252
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5831..5944
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5271..5830
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3450..3938
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4123..5042
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3939..4122
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3258..3449
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RESULT 6
US-09-453-702B-111/c
US-09-453-702B-111/c
; Sequence 111, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 215-965-1284
TELEFAX: 215-567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 18609 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local
Matches (
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,731
FILING DATE: 03-OCT-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/212,322
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,322
FILING DATE: 14-MAR-1994
PRIOR APPLICATION NUMBER: US 07/803,628
FILING DATE: 03-DEC-1991
ATTORNEY/AGENT INFORMATION:
AMPE: DOYLE LEARY Ph.D., KATHRYN
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 37-08-27
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHNOE: 215-965-1284
TELEPHONE: 215-965-1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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TOPOLOGY: linear
MOLECULE TYPE: DNA
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APPLICANT: PACK, MICHAEL
APPLICANT: COLIGE, ALAIN
APPLICANT: EARLY, JAMES
APPLICANT: KORKKO, JARMO
APPLICANT: KORKKO, JARMO
APPLICANT: ALA-KOKKO, LEENA, et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
NUMBER OF SEQUENCES: 666
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ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET,
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53.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 31.4; DE; Pred. No. 5.7; O; Mismatches
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APPLICANT: Blattner, Burland,

Frederick R. Valerie

Perna,

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TYPE: nucleic acid
;
STRANDENNESS: double
;
TOPOLOGY: linear
;
MOLECULE TYPE: DNA (genomic)
;
SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-09-453-702B-111
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                                                                                                                                                                                                    Sequence 2813, Application US/09621976 Patent No. 6639063 GENERAL INFORMATION:
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Best Local S
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                        APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENERT.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 111: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        12494 CATGCTGGAA 12485
                                                                                                                                                                                                                                                                                                                                                                                                                                        12554 AAGTTTGGTTGAAATAGGATTGGGCGCAAATATTGGAAAAAGGGTTGACAATTCCCCAT 12495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12614 ATTAATGGTAATAAATTACATAAGAAAGCAGCCAAAAAGTTAAACAGTAAAATAATTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157 NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                               296 AATGAGGGAA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 ATAAAAGGAAATGTTTGTTGAAGGCAAGCATCAGACCACTTGCACCATCCAATCACGAAC
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83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.8%;
Similarity 52.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAACACGAGATCGAACTATCATACTGAGCCAATGGTTGTAAAGGGCAGATGCTATCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SUGMEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (608) 251-501 TELEFAX: (608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 21119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 53701-2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Welch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plunkett,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicole T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30.8; D
Pred. No. 10;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 21119;
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APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REPERRICE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: DCT/FP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
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US-10-204-708-45/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: 235.
US-09-621-976-2813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 45, Application US/10204708 Patent No. 6677731 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 98
SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                              PEATURE:
NAME/KEY: unsure
LOCATION: (76, 178..179, 273, 586, 648, 651,
OTHER INFORMATION: n is a or g or c or t
                          NAME/KEY: unsure LOCATION: (1264,
                                                                                                                                                                  FEATURE: OTHER INFORMATION: chemically treated genomic DNA
                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                      LENGTH: 19233
TYPE: DNA
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LOCATION: (1264, 1267, 1559, 1607, 1677, 1703, 1742, 1848, 1850, 2033)
OTHER INFORMATION: n is a or g or c or t
                                                                     FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity hes 28; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 AYYRSMMYWWRYRCWKKKAYYRKTTCYSSKGWTWWKRWKKAWTTWWWKKTYYWAATRYWW 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 RWRGWATGAGMKAWRASCMMRRKYAGKSKTSYKSMWMCWTRSWKYCYTKARWTGYYCYRK 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 ATTTCGCTGATATCATTTCTCGGAATCGGCATCAAGAGCAGGCTCATAAACCATAAAAGG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 ACTGCCATATTAGCTTCTGTAATCATGCTTGCTTGCCTTAGCCGCCATTGTACTTGATAT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AWRWWAMWWAWRRACAAAATATAA 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative 120; Mismatches 116;
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10.6%; Pred. No. 1.8;
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                                                                                                                  920,
                                                                                                                  1014, 1173, 1197, 1228)
                                                                                                                                                                                     (Homo sapiens)
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US-09-198-452A-1
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Sequence 1, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, frac
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis,
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-99
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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NAME/KEY: unsure
NAME/KEY: unsure
(6244, 6288, 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (19200)
OTHER INFORMATION: n
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LOCATION: (19200)
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LOCATION: (18130, 1
OTHER INFORMATION:
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NAME/KEY: unsure
LOCATION: (13846,
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LOCATION: (8059, 80
OTHER INFORMATION:
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LOCATION: (10005, :
OTHER INFORMATION:
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LOCATION: (11703,
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LOCATION: (4298,
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LOCATION: (5690,
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                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                    16956 ATAAAAAATCACGAAATCAAAAAATTAAAACCATCC 16920
                                                                                                                                                                                                                                                                       229 CACGAACAAACACGAGATCGAACTATCATACTGAGCC 265
                                                                                                                                                                                                                                                                                                                                    169 ATAAACCATAAAAGGAAATGTTTGTTGAAGGCAAGCATCAGACCACCTTGCACCATCCAAT
                                                                                                                                                                                                                                                                                                                                                                                 55;
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(4787,
                                                                                                                                                                                                                                                                                                                                                                             Conservative
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N: n is a
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N: n is a or g or c or t
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N: n is a
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s a or
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is a or
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a or g or c or t
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a or g or c or t
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                                                                                                                                                                                                                                                                                                                                                                         Score 30.4; D
Pred. No. 13;
0; Mismatches
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g or c or t
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g or c or t
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                                                                                                                                                                                                                                                                                                                                                                           42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13564, 13764..13765, 13787)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5913,
                                                                                                                                                                                                                                                                                                                                                                                                          Length 19233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7876,
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NAME/KEY: misc feature
LOCATION: (285001)...(300000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc feature
LOCATION: (300001)...(315000)
OTHER INFORMATION: n=a or c or
                                                                                                                                                                                                                                                            NAME/KEY: mlsc_feature
LCCATION: (180001)...(195000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: mlsc_feature
LCCATION: (195001)..(210000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: mlsc_feature
LCCATION: (210001)..(225000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: mlsc_feature
LCCATION: (210001)..(225000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: mlsc_feature
LCCATION: (225001)..(240000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (13501)..(15000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc feature
LOCATION: (15001)..(16500)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc feature
LOCATION: (165001)..(18000)
OTHER INFORMATION: n=a or c or
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SEQ ID NO 1
                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (25501)..(270000)
OTHER INFORMATION: n=a or c
COTHER INFORMATION: n=a or c or g
                              NAME/KEY: misc
                                                                                                                                 LOCATION: (270001)..(285000)
OTHER INFORMATION: n=a or c
                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (240001)..(255000)
OTHER INFORMATION: n=a or c
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LOCATION: (105001)..(120000)
OTHER INFORMATION: n=a or c
NAME/KEY: misc feature
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DTHER INFORMATION: n=a or c
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NAME/KEY: misc_feature
LOCATION: (90001)..(105000)
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OTHER INFORMATION: n=a or c
NAME/KEY: misc feature
LOCATION: (60001).. (75000)
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OTHER INFORMATION: n=a or
NAME/KEY: misc_feature
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OTHER INFORMATION: n=a or
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OTHER INFORMATION: n=a or
NAME/KEY: misc_feature
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LOCATION: (75001)..(90000)
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NAME/KEY: misc feature
LOCATION: (45000)...(465000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc feature
LOCATION: (46501)...(480000)
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LOCATION: (435001)..(450000)
OTHER INFORMATION: n=a or c or g
OTHER infoRMATION: n=a or c or g
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LOCATION: (675001) ...(675000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: misc feature
LOCATION: (675001) ...(690000)
                                                                                                                   AME/KEX: "155501)..(57000)
LOCATION: (55501)..(57000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: misc feature
NAME/KEY: misc feature
1.0CATION: (57001)..(585000)
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LOCATION: (345001)..(36000
OTHER INFORMATION: n=a or
                                                                                             LOCATION: (645001)..(660000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (615001)..(630000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: misc_feature
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LOCATION: (600001)..(615000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (420001)..(435000)
OTHER_INFORMATION: n=a or c or g or t
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*^^aTTON: (405001)..(420000)
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OTHER INFORMATION: n=a or c or
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LOCATION: (645001)...
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OTHER INFORMATION: n=a or c
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OTHER INFORMATION: n=a or c or g
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THER INFORMATION: n=a or c or g or
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THER INFORMATION: n=a or c or g or t
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THER INFORMATION: n=a or c or g
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OCATION: (495001)
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Best Local S
Matches 61
                                                                           GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOUNDS AND METHODS
TITLE OF INVENTION: OF COLON CANCER
FILE REFERENCE: 210121.471
CURRENT APPLICATION NUMBER: US/09/221,298
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 77
                                                                                                                                                        Sequence 77, Application US/09221298
Patent No. 6284241
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (870001)..(885000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: misc feature
LOCATION: (885001)..(900000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: misc feature
LOCATION: (900001)..(915000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (810001)..(825000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: misc_feature
LOCATION: (825001)..(840000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (720001)..(735000)
OTHER INFORMATION: n=a or c o:
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LOCATION: (735001)..(750000)
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LOCATION: (840001). (855000)
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LOCATION: (855001). (870000)
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OTHER INFORMATION: n=a or c
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NAME/KEY: misc_feature
LOCATION: (765001)..(780000)
COTHER INFORMATION: n=a or c
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                                                                                                               THERAPY AND DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                Length 1230025;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (450) -
; OTHER INFORMATION: Where n is a, US-09-221-298-77
                                                SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 77
                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                       Sequence 77, Application US/09401064
Patent No. 6623923
                                                                                  CURRENT APPLICATION NUMBER: US/09/401,064
CURRENT FILING DATE: 1999-09-22
                                                                                                     APPLICANT: Meagher, Madeline Joy
APPLICANT: Meagher, Madeline Joy
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C2
                                                                                                                                                                                  APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Becrist, Heather
APPLICANT: Berson, Darin R.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                       NUMBER OF SEQ ID NOS:
      ORGANISM: Homo sapien
                        TYPE: DNA
FEATURE:
                                    ENGTH: 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (447)
OTHER INFORMATION: Where n is
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OTHER INFORMATION: Where n
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LOCATION: (409)
OTHER INFORMATION: Where
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LOCATION: (417)
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OTHER INFORMATION: Where
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OTHER INFORMATION: Where
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OTHER INFORMATION: Where n
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FEATURE:
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                                                                                                                                                                                                                                       INFORMATION:
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Pred. No. 1.4;
D; Mismatches 54;
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                                                                                                                                                                  Query Match
Best Local Similarity
Matches 112; Conserv
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                                                                                                                                                                                                                                                                                                                           TELEFAX: (301) 309-85 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: HP Vectra 486/3
OPERATING SYSTEM: MSDOS V
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08
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                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 10711 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (1)...(458)
OTHER INFORMATION: n = A,T,C
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and NUMBER OF SEQUENCES: 391
                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: 111
                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                              5865 ATTTGAGACGTCCGCTCCAGTTGTAAAGAAGGCGTACATGTTTTGGAAGTAACTTGTATC 5806
                                                                                            5925 ACGAATTTCATCAAAGTAAGTTGCTTGATCACCAGCTTCACGACTCAATGTCAGAGTAAC 5866
330 GGCTATATAAGCCAGGTGCATCTCTTGCTCGGGGTCGCCGTCCTACACATTGTTGTGACG 389
                                                         270 GTTGTAAAGGGCAGATGCTATCCTCCAATGAGGGAAAATGTCATGCAACATCCTGTAAGC 329
                                                                                                                         210 ACCACTTGCACCATCCAATCACGAACAACACGAGATCGAACTATCATACTGAGCCAATG 269
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48.5%;
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                                                                                                                                                           Score 30.2; DB 4;
Pred. No. 11;
0; Mismatches 118;
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Pred. No. 1
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RESULT 13
US-08-816-346-5
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                                                                                                                                                                                                       RESULT 14
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Best Local Sin
Matches 57;
                                                                                                  Sequence 5, Application US/09335411 Patent No. 6153435
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FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
REPERENCE/DOCKET NUMBER: 67167
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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ZIP: 60601-6780

ZIP: 60601-6780

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

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GENERAL INFORMATION:
APPLICANT: Crysta
APPLICANT: Falck-
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TELEX: 25-3533
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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CORRESPONDENCE ADDRESS:
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STRANDEDNESS: doub
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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TWO PRUDENTIAL PLAZA - 4900
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Crystal, Ronald G. Falck-Pedersen, Erik
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Pred. No.
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RESULT 15
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Best Local Similarity
                                                                                                                                                                                                                                                                        Patent No.
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                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                         NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 15
MOLECULE TYPE:
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LENGTH: 603 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 67
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/616-5600
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ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WICKHAM, THOMAS J.
TITLE OF INVENTION: CHIMERIC ADENOVIRAL COAT PROTEIN AND
TITLE OF INVENTION: METHODS OF USING SAME
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEVELG, VOIT & MAYER, LTD.
STREET: TWO PRUDENTIAL PLAZA - 4900
                                                                                                                                          TITLE OF INVENTION:
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APPLICATION NUMBER:
COMPUTER READABLE FORM:
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                                             STREET: TWO PR
CITY: CHICAGO
STATE: ILLINOI
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                            COUNTRY: USA
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STREET: TWO PRUDENTIAL
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                                                                                            ADDRESSEE:
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             60601-6780
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                                             ILLINOIS
                                                                        3: LEYDIG, VOIT
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Wickham,
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                                                                                                                                                                                                          Jason
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                                                                                                                                         Thomas J.
CHIMERIC ADENOVIRAL COAT PROTEIN
METHODS OF USING SAME
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                                                                                          VOIT & MAYER,
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Pred. No. 2;
                                                                              R, LTD
4900
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: DC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APELICATION NOTA;
APELICATION NUMBER: US/08/816,346
FILLING DATE: 30
ATTORNST/AGENT INFORMATION:
REFERENCE 312/616-5000
TELEENA: 312/616-5000
TELEEX: 2-533
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2907 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
WOLECULE TYPE: DNA (genomic)
US-08-816-346-1

Query Match
STRANDEDNESS: double
TOPOLOGY: Linear
WOLECULE TYPE: DNA (genomic)
US-08-816-346-1

Query Match
STRANDEDNESS: double
TOPOLOGY: Linear
WOLECULE TYPE: DNA (genomic)
US-08-816-346-1

Query Match
STRANDEDNESS: double
TOPOLOGY: Linear
WOLECULE TYPE: DNA (genomic)
US-08-816-346-1

Query Match
STRANDEDNESS: double
TOPOLOGY: Linear
WOLECULE TYPE: DNA (genomic)
US-08-816-346-1

Query Match
STRANDEDNESS: double
TOPOLOGY: Linear
WOLECULE TYPE: DNA (genomic)
US-08-816-346-1

Query Match
STRANDEDNESS: double
TOPOLOGY: Linear
WOLECULE TYPE: DNA (genomic)
US-08-816-346-1

Query Match
STRANDEDNESS: double
TOPOLOGY: Linear
WOLECULE TYPE: DNA (genomic)
US-08-816-346-1

Query Match
STRANDEDNESS: double
TOPOLOGY: Linear
WOLECULE TYPE: DNA (genomic)
US-08-816-346-1

Query Match
STRANDEDNESS: double
TOPOLOGY: Linear
WOLECULE TYPE: DNA (genomic)
US-08-816-346-1

Query Match
STRANDEDNESS: double
TOPOLOGY: Linear
WOLECULE TYPE: DNA (genomic)
US-08-816-346-1

Query Match
STRANDEDNESS: double
TOPOLOGY: Linear
WOLECULE
TYPE: TOPOLOGY: Linear
WOLECULE
TYPE
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Gapop 10.0 , Gapext 1.0
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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                                                                        2 6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
2 6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
2 6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2 6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2 6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
2 6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
2 6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                               6/ptodata/1/pubpna/US08 NEW PUB.seq:*
6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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7145.545 Million cell updates/sec
                              NEW_PUB.seq:
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the predicted by chance to have the score of the result being pure total score distribution.	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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34	35	35	35	35	35	35	35	35	35	35	35	35	35	Score
6.4	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	Query Match
616	328	328	328	328	328	328	328	328	328	328	328	328	328	Query Match Length
13	16	16	16	16	16	16	15	15	15	15	15	15	13	BB
US-10-142-426-206	US-10-140-864-34	US-10-140-805-34	US-10-141-759-34	US-10-141-756-34	US-10-140-923-34	US-10-137-871-34	US-10-158-790-34	US-10-142-885-34	US-10-141-761-34	US-10-140-472-34	US-10-146-731-34	US-10-123-155-34	US-10-142-426-34	ID
Sequence 206, App	Sequence 34, Appl	•	•	Sequence 34, Appl	•	•	•	Sequence 34, Appl	Description					

Query Match 6.6%; Score 35; DB 13; Length 328; Best Local Similarity 6.9%; Pred. No. 0.67;

4.5	C 44		42	41	c 40		38	37	36	35	34	33	32	31	30	29	c 28		26	25	24	23	22	21	20	19	18	17	16	15
31.4	w	w	w	32.2	32.	32.	32.	32.	32.	32.	32.		32.	32.	32.		33.	33.4		w						34		34	34	34
5.9	6.0			6.0		6.0	6.1	6.1	6.1	6.1		6.1		6.2		6.2				6.4			6.4			6.4	6.4			6.4
601	397658	9347	1919	20346	3410	3388	96595	650	650	650	650	650	650	25519	802	802	6617	6617	616	616	616	616	616	616	616	616	616	616	616	616
13	9	15	13	15	16	13	12	16	16	16	13	13	13	13	15	15	15	13	16	16	16	16	16	16	15	15	15	15	15	15
US-10-027-632-89624	US-09-813-320-3	US-10-204-708-36	US-10-424-599-27873	US-10-123-965B-1	US-10-120-988-225	US-10-416-592-8	US-10-052-482-232	7-632-	US-10-027-632-1040	US-10-027-632-1039	US-10-027-632-1041	US-10-027-632-1040		US-10-087-192-1207	US-10-184-634-312	US-10-184-644-312	US-10-210-296-1	US-10-449-462-1		US-10-140-805-206	US-10-141-759-206	US-10-141-756-206	US-10-140-923-206	US-10-137-871-206	US-10-158-790-206	US-10-142-885-206	US-10-141-761-206	US-10-140-472-206	US-10-146-731-206	US-10-123-155-206
Sequence 89624, A	Sequence 3, Appli	Sequence 36, Appl	N		225		Sequence 232, App	e 104	e 1040;	Seguence 1039, Ap	1041,	1040,	1039,	1207,	312,	31	1,	ļ	206,	Sequence 206, App	206,	206,	206,	206,	206,	206,	•	æ	•	Sequence 206, App

ALIGNMENTS

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; TYPE: PRT; ORGANISM: Homo Sapien US-10-142-426-34
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US-10-142-426-34/c
                                                         Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 34
LENGTH: 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 34, Application US/10142426
Publication No. US20040048333A1
                                                                                                                                         APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C224
CURRENT APPLICATION NUMBER: US/10/142,426
CURRENT FILING DATE: 2002-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Baker, Kevin P.
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Stewart, Timothy A.
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Gerritsen, Mary E.
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Watanabe, Colin K
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Filvaroff, Ellen
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US-10-123-155-34
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US-10-123-155-34/c
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CURRENT FILING DATE: 2002-04-15
Prior Application removed - See Palm or F:
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 34
LENGTH: 328
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Best Local &
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C30
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                              161 GCAGGCTCATAAACCATAAAAGGAAATGTTTGTTGAAGGCAAGCATCAGACCACTTGCAC 220
                                                                    322 BYR..M.TYNN.GHMC.
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KYA.RB.MNK..WSTA.RG...AKSCHRA..SSA..R...N.C...RTHNMRA.YA.AH
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                                                             ..S.N.NAY.GYNN...B.Y.NHSKS....S..N.S..Y.SDK.
                                                                                                                          98; Mismatches 184;
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CURRENT APPLICATION NUMBER: US/10/146,731

CURRENT APPLICATION UNMBER: US/2-05-15

Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550

SEQ ID NO 34

LENGTH: 328

TYPE: PRT
ORGANISM: Homo Sapien

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; Sequence 34, Application US/10146731
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142 C.SH.SC.D.Y....YDSRAK.CCS.NB.D.MH.Y.SBDYCANRKACSBMYCCAN.Y..A
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CURRENT FILING DATE: 2002-05-06
Prior Apploication removed - See File Wrap
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 34
SEQ ID NO 34
SEQ ID NO 34
SEQ ID NO 36
TYPE: PRT
ORGANISM: Homo Sapien
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                                                                  ...H..KDSA..NB.S.YMCBSG.NWTSNB.CW.S.B.B.SC.BB.MRTWWC.D.M.SN.
                                                                                                  CCAGGTGCATCTCTTGCTCGGGGTCGCCGTCCTACACATTGTTGTGACGTGCGGCCCAGA
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.TS 20
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No. US20030138888A1
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Wood, William
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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US-10-142-885-34/c

Sequence 34, Application US/10142885 Publication No. US20030157604A1 GENERAL INFORMATION:

APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maur. APPLICANT: DeForge, Laura

Beresini, Maureen DeForge, Laura

APPLICANT:

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; TYPE: PRT
; ORGANISM: Homo
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 34
LENGTH: 328
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Publication No. US20030148432A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
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Best Local Similarity
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C198
CURRENT APPLICATION NUMBER: US/10/141,761
CURRENT FILING DATE: 2002-05-08
CURRENT FILING DATE: 2002-05-08
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                                                                                                  341 CCAGGTGCATCTCTTGCTCGGGGTCGCCGTCCTACACATTGTTGTGACGTGCGGCCCAGA 400
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                                                                ...H..KDSA..NB.S.YMCBSG.NWTSNB.CW.S.B.B.SC.BB.MRTWWC.D.M.SN.
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.TS 20
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Wood, William
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Godowski, Paul J.
Gurney, Austin L.
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Pred. No. 0.67;
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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Mauree
APPLICANT: DeForge, Laura
APPLICANT: Desonyers, Luc
APPLICANT: Filvaroff, Ellei
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US-10-158-790-34/c
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LENGTH: 328
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ORGANISM: Homo
-10-142-885-34
                 APPLICANT:
                                APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/142,885
CURRENT FILING DATE: 2002-05-10
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                                           Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
Stewart, Timothy A
                Smith, Victoria
                           Sherwood, Steven
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Gerritsen, Mary E.
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Gurney, Austin L.
Sherwood, Steven
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Pred. No. 0.67;
98; Mismatches
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RESULT 8
US-10-137-871-34/c
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CURRENT FILING DATE: 2002-05-30
Prior Application removed - See File Wrapp
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 34
LENGTH: 328
TYPE: PRT
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APPLICANT:
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Best Local Similarity
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C153

CURRENT APPLICATION NUMBER: US/10/137,871

CURRENT FILING DATE: 2002-05-03
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APPLICANT:
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APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C448
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Wood, William
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Godowski, Paul J.
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Filvaroff, Ellen
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; ORGANISM: Homo Sapien
US-10-137-871-34
                                     US-10-140-923-34
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NUMBER OF SEC ID NOS: 550
SEC ID NO 34
LENGTH: 328
                                                                                      Prior Application removed -
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 34
LENGTH: 328
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Best Local Similarity 6.9%;
Matches 21; Conservative
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CURRENT APPLICATION NUMBER: US/10/140,923
CURRENT FILING DATE: 2002-05-07
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ORGANISM: Homo Sapien
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; Pred. No. 0.67;
98; Mismatches 184; Indels
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US-10-141-756-34/c
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US-10-141-756-34
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 34
LENGTH: 328
TYPE: PRT
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 9330R1C200
CURRENT APPLICATION NUMBER: US/10/141,756
CURRENT FILING DATE: 2002-05-08
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nes 21; Conserv
322 BYR. M. TYNN. GHMC. .S.N.NAY. GYNN. .. B.Y.NHSKS. ...S..N.S..Y.SDK. 263
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                                                                                                                   6.6%; Score 35; DB ilarity 6.9%; Pred. No. 0.67; Conservative 98; Mismatches
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                                                                                                                                      DB 16; Length 328.67;
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CURRENT FILING DATE: 2002-05-08
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 34
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-10-141-759-34
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US-10-141-759-34/c
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Publication No. US20030207361A1
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nes 21; Conservative
142 C.SH.SC.D.Y....YDSRAK.CCS.NB.D.MH.Y.SBDYCANRKACSBMYCCAN.Y..A 83
                            281 CAGATGCTATCCTCCAATGAGGGAAAATGTCATGCAACATCCTGTAAGCGGCTATATAAG 340
                                                        202 YN.KYN...NSSHSEM...SBBB.CN.SMTT.ABNAR..DNRD...B.CS.T.CN..D.S
                                                                                     221 CATCCAATCACGAACAAACACGAGATCGAACTATCATACTGAGCCAATGGTTGTAAAGGG 280
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Watanabe, Colin K
Wood, William
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Gerritsen, Mary E.
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Pred. No. 0.67;
98; Mismatches 184; Indels
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US-10-140-805-34
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US-10-140-805-34/c
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 34
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Best Local
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C176
CURRENT APPLICATION NUMBER: US/10/140,805
CURRENT FILING DATE: 2002-05-07
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APPLICANT:
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Publication No. US20030207417A1
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TYPE: PRT
ORGANISM: Homo Sapien
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21; Conservative 9
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.TS 20
                               TTC 403
                                                      ...H..KDSA..NB.S.YMCBSG.NWTSNB.CW.S.B.B.SC.BB.MRTWWC.D.M.SN.
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Wood, William
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Gurney, Austin L.
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Pred. No. 0.67;
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US-10-142-426-206
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US-10-140-864-34/c
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APPLICANT: Beresini, Mauree
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
                                                            Sequence 206, Application US/10142426 Publication No. US20040048333A1 GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C184
CURRENT APPLICATION NUMBER: US/10/140,864
CURRENT FILING DATE: 2002-05-07
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ORGANISM: Homo Sapien
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                                                                                                                                                                                                                                                                                                                          341 CCAGGTGCATCTCTTGCTCGGGGTCGCCGTCCTACACATTGTTGTGACGTGCGGCCCAGA 400
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SEQ ID NO 206
LENGTH: 616
TYPE: PRT
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CURRENT FILING DATE: 2002-05-09
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                    SETETTEAIDDEGWLHSGDLGQLDGLGFLYVTGHIKEILITAGGENVPPIPVETLVKK 485
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                                                                                                          ELYGLSESSGPHTISNONNYRLLSCGKILTGCKNMLFQQNKDGIGEICLWGRHIFMGYLE
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Watanabe, Colin K
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Sequence 206, Application US/10123155 Publication No. US20030068794A1 GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Mauro
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc

Beresini, Maureen DeForge, Laura

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; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-123-155-206
Search completed: May 25, 2004, 03:05:08 Job time : 341 secs
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Best Local Similarity 9.6%; Pred. No. 2.1;
Matches 46; Conservative 124; Mismatches 308; Indels
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CURRENT FILING DATE: 2002-04-15
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K
Wood, William
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                                                                            SETETTEAIDDEGWLHSGDLGQLDGLGFLYVTGHIKEILITAGGENVPPIPVETLVKK 485
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Godowski, Paul J.
Gurney, Austin L.
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Maximum DB
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38.2 7.2
37.8 7.1
37.4 7.0
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Gapop 10.0 , Gapext 1.0
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AL564823	AL564823		1200		ω.	43
AL29029	CNS04GZL		892		ω	42
AQ37228	AQ372284		693	٠	ω.	41
BH76578	BH765785		623	6.3	·	40
BQ70168	BQ701682		549	6.3	u	39
BG27567	BG275671		494		ω.	38
CE523584 tigr-gss-	CE523584		429		33.8	37
AV654960	AV654960		370		ω	36
CG24850	CG248509		898		34	35
CG24850	CG248501		850		34	34
CE73719	CE737197		559		34	ω ω
AZ16449	AZ164493		479			32
CG67475	CG674752		838		4	3
AQ88863	AQ888634		740		4	30
BZ95307	BZ953077		616	6.4	Δ	29
CA87119	CA871192		543		4	28
AQ35985	AQ359853		500		4	27
AQ41013	AQ410136		384		4	26
AA504855	AA504855		539		4	25
AL514124	AL514124		1201	٠	4	24
AL10701	CNS016OP		1101		34.6	23
BZ035991 oeh99e02.	BZ035991	28	707		4	22
AQ641009 927P1-3B6	AQ641009	28	458	•	4	21
AQ63882	AQ638821		456		•	20
BX41520	BX415200		1040		35	19
BZ99257	BZ992571		787		35	18
AQ31884	AQ318844		584	٠		17
AL06035	CNS00D88		1101		(n	16
AL06805	CNS00L9Z		962		ιn	15
CG92864	CG928645		ū		tn.	14
BZ069169	BZ069169		798	٠	LD.	13
BH567971	BH567971		ø		LD.	12
BI30847	BI308473		w		ĽП	11
BI350586	BI350586	12	456	6.6	35.4	10
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AL07368	CNS00HK4		999		O	œ
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5 Danio r	45	29	745	6.9	37	u

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	REFERENCE AUTHORS TITLE JOURNAL COMMENT	VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 AL549619 LOCUS DEFINITION
Contact: Genoscope Genoscope - Centre National de Sequencage Bp 191 9106 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 8081.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CS0DI055AE070P1&cluster=8081.r. Contact: Feng Liang Email: fliang@lifetech.com URL:	mammalia; Eutheria; Frimates; Catarrhin; Hominidae; Homo. 1 (bases 1 to 1201) Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001) On Feb 15, 2001 this sequence version replaced gi:12885780.	AL549619.2 GI:31271437 AL549619.2 GI:31271437 HOMO sapiens (human) Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	AL549619 1201 bp mRNA linear EST 31-MAY-2003 AL549619 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA Clone CSODI055XI13 5-PRIME, mRNA sequence.

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BMBAC372H04T7 PSU Brugia malayi Genomic Bac
genomic, genomic survey sequence.
BH767965
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                                                                                                                                                                                                                            Sequenced from the Brugia malayi BAC library constructed by Claire Whitton and Dr Mike Quail. The sequence was generated by The Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in collaboration with Mark Blaxter, ICAPB, University of Edinburgh,
                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Blaxter ML
Institute of Cell, Animal and Population Biology
University of Eddinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mhitton,C., Daub,J., Ware,J., Quail,M., Hall,N., Barrell,B., Whitton,C., Daub,J., Ware,J., Quail,M., Hall,N., Barrell,B., Foster,J., Guiliano,D., Slatko,B. and Blaxter,M. Genome survey sequences from the human parasitic nematode Brugia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brugia malayi
                                                                                                                                                               Seq primer: T7 (Class: BAC ends.
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                                                                                                                                                                                                           Edinburgh, UK.
                                                                                                                                                                                                                                                                                                                          Email: mark.blaxter@ed.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
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+44 131 670 5450
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Tist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                             organism="Brugia malayi"
/mol_type="genomic DNA"
/strain="TRS"
                                                                                                                                    Location/Qualifiers
sex="Mixed (male and female)"
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                          xref="taxon:6279"
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41.3%; Pred. No. 0.83;
tive 24; Mismatches 81;
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 654)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/clone_lib="Brugia malayi Genomic BamH I; Brugia malayi
/note="Vector: pBACe3.6; Site_1: BamH I; Brugia malayi
genomic DNA was partially cleaved with Sau3A I and size
genomic DNA was partially cleaved with Sau3A I and size
fractionated. 7,392 clones were generated with mean insert
size -48 kbp. The library was constructed by Claire
Whitton, Blaxter Nematode Genetics Lab, University of
Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing
Unit, The Sanger Centre, Cambridge, UK."
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/lab_host="DH10B (phage-resistant)"
/clome_lib="NIH_MGC_90"
/note="Torgan: liver; Vector: pCMV-SPORT6; Site_1: Not1;
/note="
                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5405813"
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             601810690R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: LLCM892 row: d column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF128543.1 GI:10967583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
 CGAATCTGTAATAAAAGCTTTTTCTTCTATATCCTCAGATTGGCAGTGAGA 453
                                                                      AGGTGCATCTCTTGCTCGGGGTCGCCGTCCTACACATTGTTGTGACGTGCGGCCCAGATT 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGCAMACATAACCAMACMAGMAGMAAGAACAGAGAGACGATCGMACGA 629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCATGCTTGCCTTAGCCGCCATTGTACTTGATATATTTCGCTGATATCATTTCTC 144
                                      AAGGGGGTTTGTAGCTCGTCGTGGCGGTAGTACATATTATAGTGGCGCCCCACCCTGTTA
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                                                                                                                                                                                                       /clone="IMAGE:4053479"
/clone="IMAGE:4053479"
/tissue_type="leiomyosarcoma cell line"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 46"
/clone lib="NIH MGC 46"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
/corr; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II.RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       through the I.M.A.G.E. Consortium/LLNL
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Sutheria; Primates; Catarrhini; Hominidae; Homo.
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                                             Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
1i, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79;
   Email: seqref@genoscope.cns.fr,
                   Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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                                                                                                                                                                                                                                        BX381961.1 GI:30453007
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/mol_type="genomic DNA"

/db_xref="taxon:7955"
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Pred. No.
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   Web : www.genoscope.cns.fr
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BX381961 Homo sapiens PLACENTA COT 25-NORMALIZED Clone CSODIO72YF05 3-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was generated from the T7 end is part of the Daniokey BAC Library created Keygene. Further details:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humphray, S.J., Huckle, E. and Durham, J.L. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 745)
                                                                                                                                                                                                                                                                        CATTGTACTTGATATATTTCGCTGATATCATTTCTCGGAATCGGCATCAAGAGCAGGCTC 168
                                                                                                                                                                                                                                 GTTTTATTTAGATTTAGTTAATATTAGTTTTTGGAATTCTGTGCATTGGAAAGAAG
                                                                                                                                                                                                                                                                                                                 AGCGCTGGCTCGCTAACTGCCATATTAGCTTCTGTAATCATGCTTGCCTTGCCTTAGCCGC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="DKEY-186F13"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"
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survey sequence
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1 (bases 1 to 636)
Carlton, J.M.-R. and Dame, J.B.
The Plasmodium vivax and P. berghei gene sequence tag
Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)
Contact: Dame JB
Dept. of Pathobiology, College of Veterinary Medicine
University of Florida
                                                                                                                                                  Plasmodium vivax (malaria parasite P. vivax)
Plasmodium vivax
Eukaryota; Alveolata; Apicomplexa; Haemosporida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 ATTAGCTTCTGTAATCATGCTTGCCTTGCCTTAGCCGCCATTGTACTTGATATATTTCGCT 131
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AZ572287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="CSODI0721F05"
/tissue type="PLACENTA COT 25-NORWALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sites of the pCMVSPORT 6 vector. Library was normalized."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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ic 3', genomic
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    Direct Submission
Submitted (02-JUN-1999)
BP 191 91006 EVRY cedex
                                                                               Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musco:
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31
                                                                      Genoscope
                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genome survey sequence T7 end of BAC: BACR35P15 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88;
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Tel: 352 392 4700
Fax: 352 392 9704
Email: damej@mail.vetmed.ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: damej@mail.vetmed.ufl.edu
Seq primer: M13(~20) forward
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                                                                                                                                                                                                                                                                                     genomic survey sequence.
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lab_host="Saimiri boliviensis"
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- FRANCE (E-mail :
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National de Sequencage segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                           linear GSS 03-JUN-1999 ence T7 end of BAC:
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                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata Mammalla; Eutheria; Primates; Catarrhini; Hominida 1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
On Feb 13, 2001 this sequence version replaced gicontact: Genoscope
Genoscope - Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 ACCATCCAATCACGAACAAACACGAGATCGAACTATCATACTGAGCCAATGGTTGTAAAG 278
                                           http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODC012AG02NP1&cluster=2889.f. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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                                                                                                                                                              Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2889
more information about this cluster, see
                                                                                                                                                                                                                                                                          BP 191 91006 EVRY cedex - France

    Web : www.genoscope.cns.fr)

                    http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODC012AG02NP1.
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AL525502.2 GI:31063366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCCAGGTGCATCTCTTGCTCGGGGTCGCCGTCCTACACATTGTTGTGA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCTTAAMTWGGGTCCCAGKGMCACWAAATGGYCTCCYCCTTCCTTTAMCCGTGCCAMAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASGKTGGAAGGAACMAAAAWVNHBWRAAYTAATTAGGRAAWTGTGCCMAKGYTTTTWAAT 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Drosophila melanogaster"
/mol type="genomic DNA"
/mb xref=""eaxon.7227"
/clone="BACR35P15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone_lib="RPCI-98"
note="end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36.4;
Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 999;
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 456)

1 (bases 1 to 456)

1 (clark, M., Johnson, S.L., Tehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, Li, Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Washu Zebrafish EST Project 1998
                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: John Ngai. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: infc@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (amail contact: infc@gresgen.com) and Research Genetics i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1998)
Other_ESTs: fr33h04.x1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Danio rerio
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                                                                                                                                                                                                                                                                    www.rzpd.de)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACACGAGATCGA 249
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/tissue type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="Tist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
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/db_xref="taxon:9606"
                                                                                                                                                                               Location/Qualifiers
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37.6%;
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Pred. No. 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B395328e
TIGR seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Michael A. Grusak
USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
Tel: 713-798-7044
                                                                                                                                                                                                                                                                                                                                                                                                 TIGR sequence name: MTOAQ06TK
More information is available
Seq primer: SKmod (CTA 9AA CTA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mgrusak@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grusak,M.A., Samac,D.A., Town,C.D.,
Cho,J. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001
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BI308473.1 GI:14982800
EST.
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EST529983 GPOD Medicago truncatula cDNA clone pGPOD-7All
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ilarity 52.3%;
Conservative
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/sex="mixed male and female"
/tissue_type="brain"
/dev stage="adult"
/lab host="E. coli DH10B"
/clone_lib="zebrafish adult brain"
/note="Vector: pzIFLOX; Site_1: NotI; Site_2: SalI;
Original library was constructed in lambdaZIFLOX. Mass
excision of the cDNA library was performed to yield
pzIFLOX plasmids. Insert check was done in original
library."
/Clone="pGPOD-7All"
/tissue_type="immature pod walls"
/dev_stage="Immature pods, ranging in age from 15 to 30
/dev_stage="Immature pods, ranging in age from 15 to 30
/days after pollination"
/clone_lib="GPOD"
/clone_lib="GPOD"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Immature pods, ranging in age from 15 to 30 days
                                                                                                                                                                                                                                                                         /organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="A17"
                                                                                                                                                                                                                                            db_xref="taxon:3880"
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gtg gAT CC).
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 GAAC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                            Class: sheared ends.
                                                                                                                                                                                                                                                                Email: cdtown@tigr.org
DNA is from a doubled haploid provided by
Seq primer: TF
                                                                                                                                                                                                                                                                                                                                                                                                               Other GSSs: BOGHG05TR
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCGCCGGCGATTCCACCGCCTCGTCTCCTCCGCTCGGAGATTCTGTTATCAT-CAT 106
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                                                                                                                                                                                                                                                                                                                                                    Medical Center Drive, 301-838-3523
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/clone lib="BOGH"
/clone lib="BOGH"
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
/normic DNA inserted into pHOS1 using BstXI linkers"
                                                                                          /organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db xref="taxon:3712"
/clone="BOGHG05"
                                                                                                                                                                                                       1. .595
                                                                                                                                                                                                                       Location/Qualifiers
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57.1%;
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Pred. No. 11;
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Score 35.2;

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Best Local :
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                                                                                                                                                                                                                                                                          84 AATCATGCTTGCCTTAGCCGCCATTGTACTTGATATTTTCGCTGATATCATTTCT 143
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  MBEHF36TF mth2 Medicago truncatula genomic clone 55E24, genomic curvey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: lkh07 row: g column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whole genome shotgun reads from Brassica oleracea 
Unpublished (2002)
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Brassica oleracea
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1kh07g11.b1 B.oleracea002 Brassica
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                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="B.oleracea002"
/clone lib="Wector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea T01000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103;
                                                                        Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 962)
                                                                                                                                                                                                                                                                    CNSU019Z

962 bp

DNA

1inear GSS 03-JUN-1999

Drosophila melanogaster genome survey sequence TET3 end of BAC:

BACR24H08 of RPCI-98 library from Drosophila melanogaster (fruit
    Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre
BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Town, C.D., Shetty, J., I
Sequencing of BAC ends
Unpublished (2003)
Other_GSSs: MBEHF36TR
                                                            Genoscope
                                                                                                                                                                                               AL068054.1 GI:4958184
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cdtown@tigr.org
Seq primer: TGTAAAACGACGGCCAGT
Class: BAC ends.
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Medicago truncatula
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GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTCCAATGAGGGAAAATGTCATGCAACATCCTGTA 326
                                                                                                                                                                                                                                                                                                                                                                                                               AATCCCTATAGGCCAAGTTGCTCCCAATATCCTGTA 396
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                                                                                                                                                                                                                                                       genomic survey sequence.
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/mol_type="genotic DNA"
/cultivar="genotype A17"
/db_xref="taxon:3880"
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/note="Vector: pBeloBAC11; Site_1: HindIII;
HindIII; Cook, D.R. and Kim, D.J, unpublish
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National de Sequencage : segref@genoscope.cns.fr
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Search completed: May 25, 2004, 02:57:39 Job time: 2504 secs
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                          883 MASKTIMCMIAMAMAAATGMCYIKKKXWWAAMAACAITGMIARVAAAIKGGKCMRM 824
                                                                                                        222 ATCCAATCACGAACAAACACGAGATCGAACTATCATACTGAGCCAA 267 |: || :: | :: || :| || 823 AKRAAAGSWDRNTATWMCCDCKKRATAARMAAWWWAATDGAAVCAA 778
                                                                                                                                                                                                                                                                                                                                   943 TATMCAGKVKTRWMMTKGGKTTWTTTAGKKTTTAWGKRAKAAGAGAAANAGCCAWAHVRR 884
                                                                                                                                                                                                                                                                                                                                                                         102 TAGCCGCCATTGTACTTGATATATTTCGCTGATATCATTTCTCGGATTCGGCATCAAGAG 161
                                                                                                                                                                                                                                                                                162 CAGGCTCATAAACCATAAAAGGAAATGTTTGTTGAAGGCAAGCATCAGACCACTTGCACC 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db xref="taxon:7227"
/clone="BACR24H08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.6%; Score 35.2; D
27.7%; Pred. No. 17;
tive 52; Mismatches
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